

	Matches	3962	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	CGGGCCCTGAGACTGGGGGTACTGGAGCCTTAAGAGAACTCTGAGCTGGAGGCCCCGACAG	60							
Db	1	CGGGCCCTGAGACTGGGGGTACTGGAGCCTTAAGAGAACTCTGAGCTGGAGGCCCCGACAG	60							
QY	61	CTGCTCTGGGAGCGCCCTCCGACACCCGACCCCGCGGGCGCTCCCGCTCCCGGCTC	120							
Db	61	CTGCTCTGGGAGCGCCCTCCGACACCCGACCCCGCGGGCGCTCCCGCTCCCGGCTC	120							
QY	121	CGGGCTCTGGGCTCCCTCCGCTCCGCCGCCGCCCTCGCCCGCCGCGGCGAAGAGCCCGCT	180							
Db	121	CGGGCTCTGGGCTCCCTCCGCTCCGCCGCCGCCCTCGCCCGCCGCGGCGAAGAGCCCGCT	180							
QY	181	CCCGGGTCCGAGAGCCCTGGGTCTCGCGGGAGAAAGCCATGAGAGTGTCTGAAGTGGCTAT	240							
Db	181	CCCGGGTCCGAGAGCCCTGGGTCTCGCGGGAGAAAGCCATGAGAGTGTCTGAAGTGGCTAT	240							
QY	241	TCACCTAGAGCATGAGGGTGTGACTTGAAGAAATGCCAAGAGATGCTGCCGCCACCCCTTA	300							
Db	241	TCACCTAGAGCATGAGGGTGTGACTTGAAGAAATGCCAAGAGATGCTGCCGCCACCCCTTA	300							
QY	301	GGCCGAGGGATCAGAGACTATGGGACCAAGAGCCCTGTCACTCTTACTGTGCTGCTCT	360							
Db	301	GGCCGAGGGATCAGAGACTATGGGACCAAGAGCCCTGTCACTCTTACTGTGCTGCTCT	360							
QY	361	TGGTGCAAGTGGAGATGCTGATAGAAAGAGCAATTTGATATCTCGCAAGTCCCTCTATG	420							
Db	361	TGGTGCAAGTGGAGATGCTGATAGAAAGAGCAATTTGATATCTCGCAAGTCCCTCTATG	420							
QY	421	CCCTGGGCATGACAGGACCGACCATCCAGACAGTACATCTCTGCTCCACCTGCTGT	480							
Db	421	CCCTGGGCATGACAGGACCGACCATCCAGACAGTACATCTCTGCTCCACCTGCTGT	480							
QY	481	CAGATTCCACTCCGCCGCCACAGAGGTGGAGAGCAAGTATACGGGGATGGGGCCTGCT	540							
Db	481	CAGATTCCACTCCGCCGCCACAGAGGTGGAGAGCAAGTATACGGGGATGGGGCCTGCT	540							
QY	541	GCCCGCAGAGGTCGGTGTTCCTCAAGAGAGAGAGTACTTGCAGTGGATCTACAAACAC	600							
Db	541	GCCCGCAGAGGTCGGTGTTCCTCAAGAGAGAGAGTACTTGCAGTGGATCTACAAACAC	600							
QY	601	TCCACTGGTGGCTCTGGTGGGACACCCAGAGACGGCATGCGGGGGCCTGGGCAAGAGT	660							
Db	601	TCCACTGGTGGCTCTGGTGGGACACCCAGAGACGGCATGCGGGGGCCTGGGCAAGAGT	660							
QY	661	TCTCCCGAGCTACCGGCTGCTACTCCCGGGATGCTGCGCGTGGATGGGCTGGAAG	720							
Db	661	TCTCCCGAGCTACCGGCTGCTACTCCCGGGATGCTGCGCGTGGATGGGCTGGAAG	720							
QY	721	ACCCTGGGGGTGAGAGGTGATCTCAGGCAATGAGACCCCTGAGGAGTGTGCTGAAG	780							
Db	721	ACCCTGGGGGTGAGAGGTGATCTCAGGCAATGAGACCCCTGAGGAGTGTGCTGAAG	780							
QY	781	ACCTTGGGGCCCCCAATGGTGTGCGACTGGTGGCTTACCCCGGGGCTGACCGGGTCA	840							
Db	781	ACCTTGGGGCCCCCAATGGTGTGCGACTGGTGGCTTACCCCGGGGCTGACCGGGTCA	840							
QY	841	TGAGTGTCTGTGCGGGGTAGAGCTCTATGCTGCTCTGAGGGATGAGTCTCTGT	900							
Db	841	TGAGTGTCTGTGCGGGGTAGAGCTCTATGCTGCTCTGAGGGATGAGTCTCTGT	900							
QY	901	ACACCGCCCTTGGGGCGAGACAATGTATTTATCTGAGGCCGTGTACTCAACGACTCA	960							
Db	901	ACACCGCCCTTGGGGCGAGACAATGTATTTATCTGAGGCCGTGTACTCAACGACTCA	960							
QY	961	CCTATGAGGACATACCGTGGGCGAGCTGACATGAGGGGTCTGGGCCAGCTGGAGATG	1020							
Db	961	CCTATGAGGACATACCGTGGGCGAGCTGACATGAGGGGTCTGGGCCAGCTGGAGATG	1020							
QY	1021	GTGTGTGGGGTGGATGACTTTAGGAAGATCAGGAGCTGGGGTCTGGCCAGGCTATG	1080							
Db	1021	GTGTGTGGGGTGGATGACTTTAGGAAGATCAGGAGCTGGGGTCTGGCCAGGCTATG	1080							

QY	1081	ACAAATGTGGAGTGGAGACACACACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTGAGT	1140
QY	1081	ACTATGTGGAGATGGAGACACACACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTGAGT	1140
QY	1141	TTGACCGGCTAGAGGGCCCTCCAGAGCTATGGAGGTCCAGTAACTATACATGACACAGCTGG	1200
QY	1141	TTGACCGGCTAGAGGGCCCTCCAGAGCTATGGAGGTCCAGTAACTATACATGACACAGCTGG	1200
QY	1141	TTGACCGGCTAGAGGGCCCTCCAGAGCTATGGAGGTCCAGTAACTATACATGACACAGCTGG	1200
QY	1201	GAGCCCTGTGCTGGCGGGGTGSAATGTGCTTCGGGCGTGGCCCTGCATATGGCTGGG	1260
QY	1201	GAGCCCTGTGCTGGCGGGGTGSAATGTGCTTCGGGCGTGGCCCTGCATATGGCTGGG	1260
QY	1261	AGGGGAGCCCATGGGCGCACAACTATAGGGGGCAACCTGGGGGAGCCCCAGAGCCGGGGCTG	1320
QY	1261	AGGGGAGCCCATGGGCGCACAACTATAGGGGGCAACCTGGGGGAGCCCCAGAGCCGGGGCTG	1320
QY	1321	TCTCAGTACCCCTTGGGCGGCGGTGTGGCTGTGCTTTCGTGAGAGTGCAGCTTCTCTTTGGG	1380
QY	1321	TCTCAGTACCCCTTGGGCGGCGGTGTGGCTGTGCTTTCGTGAGAGTGCAGCTTCTCTTTGGG	1380
QY	1381	GGCCCTGGTACTCTTTCAGGCAAAATTCCTTCACTCTGTATGTGGGAACAATTCCTCTC	1440
QY	1381	GGCCCTGGTACTCTTTCAGGCAAAATTCCTTCACTCTGTATGTGGGAACAATTCCTCTC	1440
QY	1441	CGGCACTGGGAGGACACTCCCGGACACCCCGTGGCGGCGCTGGCCACCTCCACACA	1500
QY	1441	CGGCACTGGGAGGACACTCCCGGACACCCCGTGGCGGCGCTGGCCACCTCCACACA	1500
QY	1501	ACTTCAGCAGCTTGGAGCTGGAGCCGAGAGGCGCAGCAGCCCGTGGCCAAAGCCCGAGGGA	1560
QY	1501	ACTTCAGCAGCTTGGAGCTGGAGCCGAGAGGCGCAGCAGCAGCCCGTGGCCAAAGCCCGAGGGA	1560
QY	1561	GGCGGACCGGCATCTCATATGGCGCTGGCTGGGCGCAATCCGTCCTGCTGGCTGCATCA	1620
QY	1561	GGCGGACCGGCATCTCATATGGCGCTGGCTGGGCGCAATCCGTCCTGCTGGCTGCATCA	1620
QY	1621	TTGCCCCTATGCTGTGGCGGGGTGCACGTGGGCGCAGGCTCCTCAGCAAGGCTGACAGGAGG	1680
QY	1621	TTGCCCCTATGCTGTGGCGGGGTGCACGTGGGCGCAGGCTCCTCAGCAAGGCTGACAGGAGG	1680
QY	1681	TGTTGGAGAGAGACTGACGGTTCTACTCTCTCTCTCCCTGGGAGCACTATCTCATACACA	1740
QY	1681	TGTTGGAGAGAGACTGACGGTTCTACTCTCTCTCTCTCCCTGGGAGCACTATCTCATACACA	1740
QY	1741	ACCGCCAGGTCTAGAGAGGCAACCCCGGACAGAGAGCCCGGCGCTGTGGGAATCCGC	1800
QY	1741	ACCGCCAGGTCTAGAGAGGCAACCCCGGACAGAGAGCCCGGCGCTGTGGGAATCCGC	1800
QY	1801	CCCACTCCGCTCTGTGTGCCCAATGGCTCTCGTGTGCTCTCCAACTCAGGCTTACC	1860
QY	1801	CCCACTCCGCTCTGTGTGCCCAATGGCTCTCGTGTGCTCTCCAACTCAGGCTTACC	1860
QY	1861	GGCTCTCTTGGGCACTTAAAGCCGCTGCCCGTGAAGGCGGGGCGCCCGCCACACCCGCT	1920
QY	1861	GGCTCTCTTGGGCACTTAAAGCCGCTGCCCGTGAAGGCGGGGCGCCCGCCACACCCGCT	1920
QY	1921	GGGCGCAAAACCCACCAACACCCAGGCTTACAGTGGGACTATATGAGGCTGTGAAGCCAG	1980
QY	1921	GGGCGCAAAACCCACCAACACCCAGGCTTACAGTGGGACTATATGAGGCTGTGAAGCCAG	1980
QY	1981	GGCGCCCGCTTCTGCCCCCAGCTTCCAGAAAGGCTCCCCCATTAATGCGAGGCTGACA	2040
QY	1981	GGCGCCCGCTTCTGCCCCCAGCTTCCAGAAAGGCTCCCCCATTAATGCGAGGCTGACA	2040
QY	2041	TTGTATACCTCTCAGAGGGGTACCGGGGGCAACACTATCTGTGCTGACATGCCCCAG	2100
QY	2041	TTGTATACCTCTCAGAGGGGTACCGGGGGCAACACTATCTGTGCTGACATGCCCCAG	2100
QY	2101	GGGCACTGGGGATGGGCCCCCGCAGATGGATTTCCCTCGATCTCGACTCCGCTTCAAG	2160
QY	2101	GGGCACTGGGGATGGGCCCCCGCAGATGGATTTCCCTCGATCTCGACTCCGCTTCAAG	2160

QY 2161 AGAAGCTGGCGAGGCGCAGTTTGGGAGGTGACCTGTGTGAGCTGACAGCCCTTAAG 2220
 |||||
 Db 2161 AGAAGCTGGCGAGGCGCAGTTTGGGAGGTGACCTGTGTGAGCTGACAGCCCTTAAG 2220
 QY 2221 ATCTGCTGACGCTTGTATTTCCCTTTAATGTGCGTAAGGAGACCCCTTGTCTGGTACTG 2280
 |||||
 Db 2221 ATCTGCTGACGCTTGTATTTCCCTTTAATGTGCGTAAGGAGACCCCTTGTCTGGTACTG 2280
 QY 2281 TCAGAGTCTTACGGCGAGATGCCAGACAGAAATGCCAGCTTCTCTTGTCTCCAGAGATG 2340
 |||||
 Db 2281 TCAGAGTCTTACGGCGAGATGCCAGACAGAAATGCCAGCTTCTCTTGTCTCCAGAGATG 2340
 QY 2341 ATTTCTGAAGAGGAGATCATATGTCAGAGTCAAGGACCCCAATCATTTGCGCTGC 2400
 |||||
 Db 2341 ATTTCTGAAGAGGAGATCATATGTCAGAGTCAAGGACCCCAATCATTTGCGCTGC 2400
 QY 2401 TGGGGCTGTGTGTGACGAGACGACCCCTGTGATGATTAATGCTGATGAGAGAGAGGCG 2460
 |||||
 Db 2401 TGGGGCTGTGTGTGACGAGACGACCCCTGTGATGATTAATGCTGATGAGAGAGAGGCG 2460
 QY 2461 ACCTCAACCAAGTTCTCTCACTGCTCCACACAGCTGAGAGACAGGACGAGGCGCCCTG 2520
 |||||
 Db 2461 ACCTCAACCAAGTTCTCTCACTGCTCCACACAGCTGAGAGACAGGACGAGGCGCCCTG 2520
 QY 2521 GGGAGGGGAGGCTGCGAGAGGCGCCACCATATGATGCTACCAATGCTGTGATGTGGCAG 2580
 |||||
 Db 2521 GGGAGGGGAGGCTGCGAGAGGCGCCACCATATGATGCTACCAATGCTGTGATGTGGCAG 2580
 QY 2581 CCCAGATGCGCTCCGCGATGCGCTATCTGCGACACTCACTAACTTTGTACATCGGAGACCTG 2640
 |||||
 Db 2581 CCCAGATGCGCTCCGCGATGCGCTATCTGCGACACTCACTAACTTTGTACATCGGAGACCTG 2640
 QY 2641 CCAGCGGAACTGCTTAAGTGGGAAAAATTTCCACATCAAAATCGCAGACTTTGGCATGA 2700
 |||||
 Db 2641 CCAGCGGAACTGCTTAAGTGGGAAAAATTTCCACATCAAAATCGCAGACTTTGGCATGA 2700
 QY 2701 GCCGGAACCTGTATGCTGGGAGCTATTACCGGTGCGAGGCGCGGCGAGTGTGCCATCC 2760
 |||||
 Db 2701 GCCGGAACCTGTATGCTGGGAGCTATTACCGGTGCGAGGCGCGGCGAGTGTGCCATCC 2760
 QY 2761 GCTGATGAGCTGCGGAGAGTGCATCTCATGAGGAAATTCACGACTCGAGTGCATGCTGG 2820
 |||||
 Db 2761 GCTGATGAGCTGCGGAGAGTGCATCTCATGAGGAAATTCACGACTCGAGTGCATGCTGG 2820
 QY 2821 CCTTTGGTGTACCTGTGGGAGGTGCTGATGCTCTGTAGGCGCCAGCCCTTTGGCGACG 2880
 |||||
 Db 2821 CCTTTGGTGTACCTGTGGGAGGTGCTGATGCTCTGTAGGCGCCAGCCCTTTGGCGACG 2880
 QY 2881 TCACCGAGCAGCAGTGCATGAGAAACGGGGGAGTTTCTCCGGAGCCAGGCGCGCAGG 2940
 |||||
 Db 2881 TCACCGAGCAGCAGTGCATGAGAAACGGGGGAGTTTCTCCGGAGCCAGGCGCGCAGG 2940
 QY 2941 TGTACTGTCCCGGCGCCTGCTGCGCGCAGGCGCTATATGAGTGTGCTGGTGTCT 3000
 |||||
 Db 2941 TGTACTGTCCCGGCGCCTGCTGCGCGCAGGCGCTATATGAGTGTGCTGGTGTCT 3000
 QY 3001 GGAAGCCGAGGTGCTGAGCAGCAGCACCCTTTTCCAGCTGCATCGGTCTCTGGCAGAG 3060
 |||||
 Db 3001 GGAAGCCGAGGTGCTGAGCAGCAGCACCCTTTTCCAGCTGCATCGGTCTCTGGCAGAG 3060
 QY 3061 ATGCACACTCAACAGGCTGTGATACACATCAGTCCCTCCCTCAGGAGGTATCCAG 3120
 |||||
 Db 3061 ATGCACACTCAACAGGCTGTGATACACATCAGTCCCTCCCTCAGGAGGTATCCAG 3120
 QY 3121 GGAAGCCAGTGAACATAAACAAGAGACACATGAGCAGCTTGCCTTCCCTCCCGA 3180
 |||||
 Db 3121 GGAAGCCAGTGAACATAAACAAGAGACACATGAGCAGCTTGCCTTCCCTCCCGA 3180
 QY 3181 CAGCCCATACCTCTATATAGGCAAGTGAAGCTGAGAGTGGGCTGGGCCACCCAGGAG 3240
 |||||
 Db 3181 CAGCCCATACCTCTATATAGGCAAGTGAAGCTGAGAGTGGGCTGGGCCACCCAGGAG 3240
 QY 3241 CTGATGCCCTTCTCCCTCTCTGAGACACCTCATGTCCCTTCTCTTCTCTCC 3300

Db 3241 CTGATGCCCTTCTCCCTCTCTGAGACACCTCATGTCCCTTCTCTTCTCTCC 3300
 |||||
 QY 3301 TAGAAGCCCTGTGCGCCACCCAGCTGTCTGTGATGGATCTCTCCACCCTCTC 3360
 |||||
 Db 3301 TAGAAGCCCTGTGCGCCACCCAGCTGTCTGTGATGGATCTCTCCACCCTCTC 3360
 QY 3361 AGCCATCCCTTGGGGAAGGTTGGGGAATATAGATATAGACTGACATGCGCCATTG 3420
 |||||
 Db 3361 AGCCATCCCTTGGGGAAGGTTGGGGAATATAGATATAGACTGACATGCGCCATTG 3420
 QY 3421 GAGCAGCTGGGCGCCACTGAGCAACACTGATTCCTGAGAGGCGCTGCGCCACTTC 3480
 |||||
 Db 3421 GAGCAGCTGGGCGCCACTGAGCAACACTGATTCCTGAGAGGCGCTGCGCCACTTC 3480
 QY 3481 TCTCTCCTGTGTCACACACTGAGACCCGACAGCTGAGAAATCTGGGGGTGAGAGACAGA 3540
 |||||
 Db 3481 TCTCTCCTGTGTCACACACTGAGACCCGACAGCTGAGAAATCTGGGGGTGAGAGACAGA 3540
 QY 3541 AGGAGAGGAAAAATGTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
 |||||
 Db 3541 AGGAGAGGAAAAATGTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
 QY 3601 CTCCTCATCACCTGAAACACTGAGCTGAGGCGGTAGCGCGCCGACCCCTGATCACC 3660
 |||||
 Db 3601 CTCCTCATCACCTGAAACACTGAGCTGAGGCGGTAGCGCGCCGACCCCTGATCACC 3660
 QY 3661 CCACTTCCCACTTGCAGTCTTGTAGTAGAAGCTTCTTAAGCCTATACCTTTCTGTGAG 3720
 |||||
 Db 3661 CCACTTCCCACTTGCAGTCTTGTAGTAGAAGCTTCTTAAGCCTATACCTTTCTGTGAG 3720
 QY 3721 TAAATTTGGGATTTGGGGGGAAGAGGAGCAAGGCGCCATAGCTTGGGCTTGAACATC 3780
 |||||
 Db 3721 TAAATTTGGGATTTGGGGGGAAGAGGAGCAAGGCGCCATAGCTTGGGCTTGAACATC 3780
 QY 3781 TCTAGTGTGCTGCGACATGATTTTCTATATATCACTGAGGCTTGTACATTTTGGG 3840
 |||||
 Db 3781 TCTAGTGTGCTGCGACATGATTTTCTATATATCACTGAGGCTTGTACATTTTGGG 3840
 QY 3841 GAGAGACACAGATTTTACATTAATATATGAGACCTAGCTTAGGCAATTTTAATCCCT 3900
 |||||
 Db 3841 GAGAGACACAGATTTTACATTAATATATGAGACCTAGCTTAGGCAATTTTAATCCCT 3900
 QY 3901 GCCTAGGAGGTATATTAAGGTTGAGTTTCCACAAAAAATTTTAATCCGGAAT 3960
 |||||
 Db 3901 GCCTAGGAGGTATATTAAGGTTGAGTTTCCACAAAAAATTTTAATCCGGAAT 3960
 QY 3961 TC 3962
 |||||
 Db 3961 TC 3962
 |||||

RESULT 2
 LOCUS A42378 3754 bp DNA 1linear PAT 06-MAR-1997
 DEFINITION Sequence 1 from Patent WO9502187.
 ACCESSION A42378
 VERSION A42378.1 GI:2297854
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 3754)
 AUTHORS Gusterson,B.A., Crompton,M.R., Mitchell,P.J., Barker,K.T.,
 Martindale,J.E., Page,M.J. and Spence,P.
 TITLE CELL GROWTH FACTOR RECEPTORS
 JOURNAL Patent: WO 9502187-A 1 19-JAN-1995;
 COMMENT CANCER RES INST (GB)
 FEATURES
 source Location/Qualifiers
 1..3754
 /organism="unidentified"
 /db_xref="taxon:32644"

CDS
142..2886
/note="unnamed protein product"
/codon_start=1
/protein_id="CAA02688.1"
/db_xref="gi:2297855"
/translation="MGPEALSSILLILLIVASGDADMKHGPDPKCYATLGNDRITPD
SDLSASSMSDSTAAHRSRLSSDDGAMCPAGSVFPKSEETLQDYLQHLVAVLIGT
QGHMAGLGKESKSRRLRYSDGRMKWMDRQEVLSIGNEDEPVVLKDLGPPMVT
ARLVREYPRADRYMSVCLNRYLTCGLMRGLLSYAPVQCTMYLSEAVLNSTYDGH
TVGGLQYGLGDLADGVLDLDEFRKSOELRVWGYDYVGMNSHSESSGVEAEFEEDR
LBAFQAMVHCNNMHTLGLARLPGVECFRRRGPAPAMNEEGRHNGHGLGPPBARAY
SVPLGSRVAFYICRRLTFAGPMLTSEISFISDYVANSPPALGCTPPAPAPMPGPP
TNPSSLEPRKQPPRVAKESPTRIILGCLVAILLILLILLIALLMLHLHRRLLSK
AKERVLEELIVHLSVPGDTILINRPFREPPYOEPRKGRPSAPCAVPSALSL
LSNPAYRLLLATYARPPRGPPTPAMAPNTWQASGDYMEPEKGLALPPPONS
VHYAEADIVTLQYVTGNTYAVPALPGVADGPDVDFPRSLRFLKFKELGEGGE
VHLCEVDSPODLVDFPLNVRKHPILVAIKLRDPAKRNANDLKKVKKIINSRLK
PNIRLLGACVODPLCMITDYMENGDILNOLPILAEKKAEGAGDQAOAPGIS
YMLILHVAOIAAGMYLATLNPVHRDLATRNCIYENETITLADGSRNLTAGDY
RYOGRVAVLPIRMANECILMGFTTHSDPWAKGVITLMEVLMKLRAPFQDLDEOYIE
NAEEFPDGRQVYLSRPPACPOGLYELMLRCWRSRESEQRPFSOLHRELAEDALNTV

BASE COUNT 712 a 1146 c 1121 g 775 t
ORIGIN

Query Match 91.5%; Score 3625.6; DB 6; Length 3754;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 3733; Conservative 0; Mismatches 14; Indels 29; Gaps 7;

QY 181 CCGGGGCGAGCGCTGGGCTGCCGGAGACGATGAGAGTGTCTGAAGTGGCTAT 240
DB 2 CCGGGGCGAGCGCTGGGCTGCCGGAGACGATGAGAGTGTCTGAAGTGGCTAT 61
QY 241 TCACAGCAGTGGGCTGGACTTGAAGCAATGCCAAGATGCTGCCACCCCTTA 300
DB 62 TCACAGCAGTGGGCTGGACTTGAAGCAATGCCAAGATGCTGCCACCCCTTA 121
QY 301 GGGCCGAGGATCAGAGACTATGGACACGAGCCCTGTCTACTTACTGCTGCTCT 360
DB 122 GGGCCGAGGATCAGAGACTATGGACACGAGCCCTGTCTACTTACTGCTGCTCT 181
QY 361 TGTGCGAAGTGAAGATGCTGACATGAAGGACATTTGATCTGCGAAGTGGCGTATG 420
DB 182 TGTGCGAAGTGAAGATGCTGACATGAAGGACATTTGATCTGCGAAGTGGCGTATG 241
QY 421 CCCTGGGATGACGAGACCGGACCATCCAGACAGTACTCTGCTTCCAGCTCTGCT 480
DB 242 CCCTGGGATGACGAGACCGGACCATCCAGACAGTACTCTGCTTCCAGCTCTGCT 301
QY 481 CAGATCCACTGGCGCGCCGACAGAGAGTGGAGACAGTGGAGGAGTGGGCGCTGCT 540
DB 302 CAGATCCACTGGCGCGCCGACAGAGAGTGGAGACAGTGGAGGAGTGGGCGCTGCT 361
QY 541 GCGCCGAGGATGAGTGTTCCTCAAGAGAGAGAGTACTTGCAGTGGATCTCAACGAC 600
DB 362 GCGCCGAGGATGAGTGTTCCTCAAGAGAGAGAGTACTTGCAGTGGATCTCAACGAC 421
QY 601 TCCACCTGCTGTGCTGTGGGACCCAGGAGCGGATCCGGGGGCTTGGGCAAGAGAT 660
DB 422 TCCACCTGCTGTGCTGTGGGACCCAGGAGCGGATCCGGGGGCTTGGGCAAGAGAT 481
QY 661 TCTCCCGGAGCTACCGGCTGCTTACTCCCGGAGTGTGGCGCTGGATGGGCTGAAG 720
DB 482 TCTCCCGGAGCTACCGGCTGCTTACTCCCGGAGTGTGGCGCTGGATGGGCTGAAG 541
QY 721 ACCGCTGGGATCAGAGTGTATCTCAGGCAATGAGGACCTGAGGAGTGGTCTGAAG 780
DB 542 ACCGCTGGGATCAGAGTGTATCTCAGGCAATGAGGACCTGAGGAGTGGTCTGAAG 601
QY 781 ACCCTGGGCCCCCAGAGTGTGGCGAGTGTCTTCAACCCCGGCTGACCGGCTCA 840
DB 602 ACCCTGGGCCCCCAGAGTGTGGCGAGTGTCTTCAACCCCGGCTGACCGGCTCA 661

QY 841 TGAAGTCTCTGCTGGGGTAGAGCTATAGGCTGCTCTGGAGGAGTGAATCTCTGCTT 900
DB 662 TGAAGCTCTCTGCTGGGGTAGAGCTATAGGCTGCTCTGGAGGAGTGAATCTCTGCTT 721
QY 901 ACACCGCCCTGTGGGCAACAAATGATTTATGTAGCCCGCTTACCTCAACGACTCCA 960
DB 722 ACACCGCCCTGTGGGCAACAAATGATTTATGTAGCCCGCTTACCTCAACGACTCCA 781
QY 961 CCTATGACGACATACCGTGGGCGAGCTGAGTATGGGGGCTGGGGCAGCTGACAGATG 1020
DB 782 CCTATGACGACATACCGTGGGCGAGCTGAGTATGGGGGCTGGGGCAGCTGACAGATG 841
QY 1021 GTGTGTGGGCTGGATGACTTATGAAAGATCAGAGCTGCGGGTCTGGCCAGGCTATG 1080
DB 842 GTGTGTGGGCTGGATGACTTATGAAAGATCAGAGCTGCGGGTCTGGCCAGGCTATG 901
QY 1081 ACATATGGGATGAGAGCAACCAACAGCTTCTCCAGTGGCTATGTGGAATGAGTTAGT 1140
DB 902 ACATATGGGATGAGAGCAACCAACAGCTTCTCCAGTGGCTATGTGGAATGAGTTAGT 961
QY 1141 TTGACCGGCTGAGGGCCTTCAGGCTATGACAGTGCACACTGAACATGACACAGCTGG 1200
DB 962 TTGACCGGCTGAGGGCCTTCAGGCTATGACAGTGCACACTGAACATGACACAGCTGG 1021
QY 1201 GAGCCGCTGTGCTGGCGGGGTGGAATGTGCTTCGGCGTGGCCCTGATGCGCTGGG 1260
DB 1022 GAGCCGCTGTGCTGGCGGGGTGGAATGTGCTTCGGCGTGGCCCTGATGCGCTGGG 1081
QY 1261 AGGGGAGGCCCATGCGCCAAACCTAGGGGGCAACCTGGGGGAGACCCCAAGAGCCGGGCTG 1320
DB 1082 AGGGGAGGCCCATGCGCCAAACCTAGGGGGCAACCTGGGGGAGACCCCAAGAGCCGGGCTG 1141
QY 1321 TCTCAGTGCCCTTGGGGCGGCTGTGGCTGCTTTCGAGTGGCGCTTCTCTTTCGCG 1380
DB 1142 TCTCAGTGCCCTTGGGGCGGCTGTGGCTGCTTTCGAGTGGCGCTTCTCTTTCGCG 1201
QY 1381 GGGCTGTGTTACTTCTTACGGAATCTCTTATCTGTATGTGTGTAACAAATCTCTCT 1440
DB 1202 GGGCTGTGTTACTTCTTACGGAATCTCTTATCTGTATGTGTGTAACAAATCTCTCT 1261
QY 1441 CGGCACTGGGAGGACCTTCCCGCAGCCCGCTGGTGGCGGCTGGCCACCTCCACCA 1500
DB 1262 CGGCACTGGGAGGACCTTCCCGCAGCCCGCTGGTGGCGGCTGGCCACCTCCACCA 1321
QY 1501 ACTTCAGCACTTGAAGCTGAGACCCAGAGCCAGC--AGCCGTGGCCCAAGGCCGAGG 1557
DB 1322 ACTTCAGCACTTGAAGCTGAGACCCAGAGCCAGCCCAAGGCCGAGG 1381
QY 1558 GAGGCCGAGCCGCTATCTATGGCTGCTGTGGTGGCATATCTCTCTGCTGCTCA 1617
DB 1382 GAGGCCGAGCCGCTATCTATGGCTGCTGTGGTGGCATATCTCTCTGCTGCTCA 1441
QY 1618 TCATTGCCCCATGCTGTGCGGCTGACACTGGGCGAGGCTCTCAGCAAGGCTGAACGA 1677
DB 1442 TCATTGCCCCATGCTGTGCGGCTGACACTGGGCGAGGCTCTCAGCAAGGCTGAACGA 1501
QY 1678 GGGTGTGGAAGAGAGCTGACAGTTCACCTCTCTGCTCCCTGGGAGACATCTCTCA 1737
DB 1502 GGGTGTGGAAGAGAGCTGACAGTTCACCTCTCTGCTCCCTGGGAGACATCTCTCA 1561
QY 1738 ACAACGGCCAGGCTCTAGAGAGCCACCCCTGTAACAGAGCCCGGCTGTGGGAATC 1797
DB 1562 ACAACGGCCAGGCTCTAGAGAGCCACCCCTGTAACAGAGCCCGGCTGTGGGAATC 1621
QY 1798 CGCCCGACCTCCGCTGCTGTGCTCCCAATGGCTGGTGTGCTCTCCAAATCCAGGCT 1857
DB 1622 CGCCCGACCTCCGCTGCTGTGCTCCCAATGGCTGGTGTGCTCTCCAAATCCAGGCT 1681
QY 1858 ACCGCTCTCTTGTGGCCACTTACGCGGCTCCCTCGAGAGCCCGGCGCCGCCACACCG 1917
DB 1682 ACCGCTCTCTTGTGGCCACTTACGCGGCTCCCTCGAGAGCCCGGCGCCGCCACACCG 1741

QY 1918 CCTGGGCCAAACCCACCAACCCAGGCTTACAGTGGGACTATATGAGCCTGAGAGC 1977
| | | | |
Db 1742 CCTGGGCCAAACCCACCAACCCAGGCTTACAGTGGGACTATATGAGCCTGAGAGC 1801
| | | | |
QY 1978 CAGGGGGCCCCGCTTGTGCCCCCACTCCCCAGAACGCTCCCCCTTATGCGGAGCTG 2037
| | | | |
Db 1802 CAGGGGGCCCCGCTTGTGCCCCCACTCCCCAGAACGCTCCCCCTTATGCGGAGCTG 1861
| | | | |
QY 2038 ACATTGTTACCTGCGAGGGGCGTACCGGGGGGCAACACCTATGCTGCTGCACTGCCCC 2097
| | | | |
Db 1862 ACATTGTTACCTGCGAGGGGCGTACCGGGGGGCAACACCTATGCTGCTGCACTGCCCC 1921
| | | | |
QY 2098 CAGGGGGAGTGGGGAGTGGGGGCCCCCAGAGTGGATTTCCTCGATCGACTCCGGTTCA 2157
| | | | |
Db 1922 CAGGGGGAGTGGGGAGTGGGGGCCCCCAGAGTGGATTTCCTCGATCGACTCCGGTTCA 1981
| | | | |
QY 2158 AGGAGAACCTTGGCGAGGGGCCAGTGGGGAGGTGCACCTGTGTAGAGTGCAGAGCCCTC 2217
| | | | |
Db 1982 AGGAGAACCTTGGCGAGGGGCCAGTGGGGAGGTGCACCTGTGTAGAGTGCAGAGCCCTC 2041
| | | | |
QY 2218 AAGATCTGCTAGTCTTATTTCCCTTAAATGTGCTAAGGAGACCCCTTGTGCTAG 2277
| | | | |
Db 2042 AAGATCTGCTAGTCTTATTTCCCTTAAATGTGCTAAGGAGACCCCTTGTGCTAG 2101
| | | | |
QY 2278 CTGTCAAGATCTTACGGCCAGATGCGACCAAGAAATGCCAGCTTCTCTTGTCTCCAGA 2337
| | | | |
Db 2102 CTGTCAAGATCTTACGGCCAGATGCGACCAAGAAATGCCAGTCTCTCTTGTCTCCAGA 2143
| | | | |
QY 2238 ATGATTTCTCTAAGAGAGGTGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTCGGC 2397
| | | | |
Db 2144 ATGATTTCTCTAAGAGAGGTGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTCGGC 2203
| | | | |
QY 2398 TGTGTGGCGTGTGTGTGAGAGAGCAGCCCTCTGTGATGATTACTGACATGAGAGAGC 2457
| | | | |
Db 2204 TGTGTGGCGTGTGTGTGAGAGAGCAGCCCTCTGTGATGATTACTGACATGAGAGAGC 2263
| | | | |
QY 2458 GCGACCTCAACCAAGTCTCTAGTGCACCAACAGCTGAGAGAGCAGCAGGAGGGGCC 2517
| | | | |
Db 2264 GCGACCTCAACCAAGTCTCTAGTGCACCAACAGCTGAGAGAGCAGCAGGAGGGGCC 2323
| | | | |
QY 2518 CTGGGGAGCGGGGAGAGGCTGCGAGAGGGGCCCAACATCAGTACCCCAATGCTGTGCTATG 2577
| | | | |
Db 2324 CTGGGGAGCGGGGAGAGGCTGCGAGAGGGGCCCAACATCAGTACCCCAATGCTGTGCTATG 2383
| | | | |
QY 2578 CAGCCCGATGCGCTCCGGGATGCGTATCTGCGACACATCACTTGTATATGAGGAGC 2637
| | | | |
Db 2384 CAGCCCGATGCGCTCCGGGATGCGTATCTGCGACACATCACTTGTATATGAGGAGC 2443
| | | | |
QY 2638 TGGCCACGCGGAACTGCTAGTGGGGAATTTACCATCAAAATGCGACACTTTGGCA 2697
| | | | |
Db 2444 TGGCCACGCGGAACTGCTAGTGGGGAATTTACCATCAAAATGCGACACTTTGGCA 2503
| | | | |
QY 2698 TGAAGCGGAGACCTATAGCTGGGAGACTATACGCTGTGCAAGGGCGGCGAGTCTGCCA 2757
| | | | |
Db 2504 TGAAGCGGAGACCTATAGCTGGGAGACTATACGCTGTGCAAGGGCGGCGAGTCTGCCA 2563
| | | | |
QY 2758 TCCGCTGATGCGCTGAGATGCACTCATGAGGGAAGTTACAGACGCGAGTACGCTGT 2817
| | | | |
Db 2564 TCCGCTGATGCGCTGAGATGCACTCATGAGGGAAGTTACAGACGCGAGTACGCTGT 2623
| | | | |
QY 2818 GGGCCTTTGGTGTGACCTGTGTGAGAGTGTGATGCTGTAGAGGCCACGCCCTTTGGG 2877
| | | | |
Db 2624 GGGCCTTTGGTGTGACCTGTGTGAGAGTGTGATGCTGTAGAGGCCACGCCCTTTGGG 2663
| | | | |
QY 2878 AGCTACCGACGAGAGGATCATGAGAAAGCGGGGAGTTCTTCCGGAGCAGAGGGCGGC 2937
| | | | |
Db 2684 AGCTACCGACGAGAGGATCATGAGAAAGCGGGGAGTTCTTCCGGAGCAGAGGGCGGC 2743
| | | | |
QY 2938 AGGTGATGCTGTCCGGCGCGCTGCTGCGCGAGGGCCATATGAGCTGATCTTCGGT 2997
| | | | |
Db 2744 AGGTGATGCTGTCCGGCGCGCTGCTGCGCGAGGGCCATATGAGCTGATCTTCGGT 2803
| | | | |
QY 2998 GCTGAGCGCGGAGTGTGAGAGCGACACCTTTTCCAGCTGATCGGTCTCTGGCAG 3057
| | | | |

Db 2804 GCTGGAGCGGGAGTGTGAGCAGCGACACCCCTTTTCCAGCTGATCCGGTCTTGGCAG 2863
| | | | |
QY 3058 AGGATGCACTCAACACGAGTGTGAATACACATGACACTGCGCTCCCTCAGGAGAGTGC 3117
| | | | |
Db 2864 AGGATGCACTCAACACGAGTGTGAATACACATGACACTGCGCTCCCTCAGGAGAGTGC 2923
| | | | |
QY 3118 CAGGGAGCCAGTACACTTAAACAAAGAGACACATGGAACCTGTG-CCCTTCCCTC 3176
| | | | |
Db 2924 CAGGGAGCCAGTACACTTAAACAAAGAGAGACATGGAACCTGTGCGCTTCCCTC 2983
| | | | |
QY 3177 CCGACAGCCCATGACCTCTAATATGAGGCAAGTGAAGTGAAGTGGGCTGGGCCACCCAG 3236
| | | | |
Db 2984 CCGACAGCCCATGACCTCTAATATGAGGCAAGTGAAGTGAAGTGGGCTGGGCCACCCAG 3039
| | | | |
QY 3237 GAGAGTGAAGCCCTTCTCCCTTCTCTGAGACACATGATGCTCCCTCCTGCTTCTC 3296
| | | | |
Db 3040 GAGAGTGAAGCCCTTCTCCCTTCTCTGAGACACATGATGCTCCCTCCTGCTTCTC 3099
| | | | |
QY 3297 TTCTAGAAAGCCCTGTGTGCGCCACCCAGCTGTCTGTGATGAGATCCTCTCCACCTC 3356
| | | | |
Db 3100 TTCTAGAAAGCCCTGTGTGCGCCACCCAGCTGTCTGTGATGAGATCCTCTCCACCCAG 3159
| | | | |
QY 3357 CTCTAGCCATCCCTTGGGGAAGGTGGGGAATATATGAGATGACACTGACATGGCC 3416
| | | | |
Db 3160 CTCTAGCCATCCCTTGGGGAAGGTGGGGAATATATGAGATGACACTGACATGGCC 3219
| | | | |
QY 3417 ATTGAGACCTTGGGCGCCCACTGAGAACACATGATTCCTGAGAGAGTGGCTGCG-CCCCA 3475
| | | | |
Db 3220 ATTGAGACCTTGGGCGCCCACTGAGAACACATGATTCCTGAGAGAGTGGCTGCGCCCCA 3279
| | | | |
QY 3476 GCTTCTCTCTCTCTCAACACTGAGCCCACTGAGTGTGAGATGTGGGGGTGAGAGAGA 3535
| | | | |
Db 3280 GCTTCTCTCTCTCTCTCAACACTGAGCCCACTGAGTGTGAGATGTGGGGGTGAGAGAGA 3339
| | | | |
QY 3536 CAGAGAGAGAGGAAATGTTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3595
| | | | |
Db 3340 CAGAGAGAGAGGAAATGTTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3399
| | | | |
QY 3596 TCTTCT 3655
| | | | |
Db 3400 TCTTCT 3459
| | | | |
QY 3656 CA-CCCCCACTCCCACTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3714
| | | | |
Db 3460 CACCCCACTCCCACTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTCT 3519
| | | | |
QY 3715 GTGAGTAAATATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3774
| | | | |
Db 3520 GTGAGTAAATATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3579
| | | | |
QY 3775 GACATCTCTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3834
| | | | |
Db 3580 GACATCTCTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3638
| | | | |
QY 3835 TTGGGGGAGAGACACAGATTTTACACTAATATATGAGACCTGAGGCAATTTTAA 3894
| | | | |
Db 3639 TTGGGGGAGAGAGACAGATTTTACACTAATATATGAGACCTGAGGCAATTTTAA 3698
| | | | |
QY 3895 TCCCTGACACTAGGACAGTAAATATATAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3950
| | | | |
Db 3699 TCCCTGACACTAGGACAGTAAATATATAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3754
| | | | |

RESULT 3
HUMRKT 3738 bp mRNA linear PRI 27-SEP-1993
LOCUS
DEFINITION Homo sapiens receptor tyrosine kinase mRNA, complete cds.
ACCESSION L11315
VERSION L11315.1 GI:403386
KEYWORDS receptor tyrosine kinase.
SOURCE Homo sapiens (library: lambda-gt11) term placenta cDNA to mRNA.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3738)
Johnston, J.D., Edman, J.C. and Rutter, W.J.
A receptor tyrosine kinase found in breast carcinoma cells has an extracellular discoidin I-like domain
Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)
93296201
JOURNAL
MEDLINE
COMMENT
FEATURES
On Sep 27, 1993 this sequence version replaced 91:307397.
location/Qualifiers
1..3738
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="term placenta"
/tissue_1ib="lambda.gtl1"
1..141
142..2883
/standard_name="discoidin I-like domain receptor tyrosine kinase"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AA02866.1"
/db_xref="GI:403387"

5'UTR
CDS

3'UTR
polyA_sltle
BASE COUNT 698 a 1140 c 1123 g 777 t
ORIGIN

Query Match 91.3%; Score 3619.2; DB 9; Length 3738;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 3716; Conservative 0; Mismatches 18; Indels 26; Gaps 6;

QY 181 CCCGGTCGACGCGCTGGCTCTGCGCGGAGAGAGAGATGAGAGTGTCTGAAGTGTCTAT 240
DB 2 CCGGGTCGACGCGCTGGCTCTGCGCGGAGAGAGATGAGAGTGTCTGAAGTGTCTAT 61
QY 241 TCACTGAGCATGGGCTGGCTTGAAGAGATGCAAGAGATGCTGCCACCCCTTA 300
DB 62 TCACTGAGCATGGGCTGGCTTGAAGAGATGCAAGAGATGCTGCCACCCCTTA 121
QY 301 GGGCCGAGGATCAGAGATGAGAGAGAGAGAGAGATGATCTTACTGCTGCTCT 360
DB 122 GGGCCGAGGATCAGAGATGAGAGAGAGAGAGAGATGATCTTACTGCTGCTCT 181
QY 361 TGGTGGCAATGAGATGCTGAGATGAGAGAGATTTGATCTCTGCCAATGCCCTATG 420
DB 182 TGGTGGCAATGAGATGCTGAGATGAGAGAGATTTGATCTCTGCCAATGCCCTATG 241
QY 421 CCCGTCGATGAGAGAGAGAGAGATGAGAGATGATCTCTGCTTCCAGTCCGCT 480
DB 242 CCCGTCGATGAGAGAGAGAGAGATGAGAGATGATCTCTGCTTCCAGTCCGCT 301
QY 481 CAGATTCTACTGCGCGCGCACAGAGAGTGGAGAGACATGACGGGATGGGCTGTG 540
DB 302 CAGATTCTACTGCGCGCGCACAGAGAGTGGAGAGACATGACGGGATGGGCTGTG 361

QY 541 GCCCGCAGAGGTCGGTCTTTCCAGAGAGAGATCTGACAGTGTATCTACACAGC 600
DB 362 GCCCGCAGAGGTCGGTCTTTCCAGAGAGAGATCTGACAGTGTATCTACACAGC 421
QY 601 TCCACCTGCTGCTCTGCTGGGACCCAGAGAGAGATGCCGGGGCTGGGACAGAGT 660
DB 422 TGCACCTGCTGCTCTGCTGGGACCCAGAGAGAGATGCCGGGGCTGGGACAGAGT 481
QY 661 TCTCCGAGATCAGAGGATGCTACTCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 482 TCTCCGAGATCAGAGGATGCTACTCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 541
QY 721 ACCGTCGGGTCAGAGAGATGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 542 ACCGTCGGGTCAGAGAGATGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
QY 781 ACCTTGGGCCCCCAGAGAGATGCTGCTGCTCTACCCCGGGCTGACCGGCTCA 840
DB 602 ACCTTGGGCCCCCAGAGAGATGCTGCTGCTCTACCCCGGGCTGACCGGCTCA 561
QY 841 TGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 662 TGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
QY 901 ACACCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 722 ACACCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
QY 961 CCTATGACGAGATACCGTGGGCGGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 1020
DB 782 CCTATGACGAGATACCGTGGGCGGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 841
QY 1021 GTGGGGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 842 GTGGGGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 901
QY 1081 ACTATGAGATGAGAGACCAACAGCTTCTCAGATGCTATGAGAGAGTGTGAGT 1140
DB 902 ACTATGAGATGAGAGACCAACAGCTTCTCAGATGCTATGAGAGAGTGTGAGT 961
QY 1141 TTGACGGGTCGAGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCC 1200
DB 962 TTGACGGGTCGAGAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCC 1021
QY 1201 GAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1022 GAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081
QY 1261 AGGGGAGAGCCATGCGCACACCACTAGGGGAGCACTGGGGGAGCCAGAGCCGGCTG 1320
DB 1082 AGGGGAGAGCCATGCGCACACCACTAGGGGAGCACTGGGGGAGCCAGAGCCGGCTG 1141
QY 1321 TCTCAGTGGCCCTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1142 TCTCAGTGGCCCTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
QY 1381 GGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1202 GGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
QY 1441 CGGCACTGGAGAGACCTTCCCGCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1262 CGGCACTGGAGAGACCTTCCCGCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
QY 1501 ACTTACGACATGAG 1560
DB 1322 ACTTACGACATGAG 1381
QY 1561 GCCGACCGGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1382 GCCGACCGGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1441
QY 1621 TTGCCCTCATGCTCTGCGGCTGCACTGGCGCAGGCTCTCAGCAGAGCTGAAAGGAG 1680

```
Db 1442 TTCCCTCATGCTCTGCGGGCTGCACGTGGCGCAGGCTCTCAGCAAGGCTGAAGGAGG 1501
Qy 1681 TGTGGAGAGAGAGTGCAGGTTCCACCTCTCTGCTCCCTGGGAGACATATCTCATACA 1740
Db 1502 TGTGGAGAGAGAGTGCAGGTTCCACCTCTCTGCTCCCTGGGAGACATATCTCATACA 1561
Qy 1741 ACCGCCAGGTCTTAGAGAGCCACCCCGTACCAGAGAGCCCGGCTGTGGGAATCCG 1800
Db 1562 ACCGCCAGGTCTTAGAGAGCCACCCCGTACCAGAGAGCCCGGCTGTGGGAATCCG 1621
Qy 1801 CCCACTCCGCTCCCTGTGTCCCAATGCGTCTGCTGTCTCTCAATCCAGCTACC 1860
Db 1622 CCCACTCCGCTCCCTGTGTCCCAATGCGTCTGCTGTCTCTCAATCCAGCTACC 1681
Qy 1861 GCTCTCTTGTGGCACTTACGCGCTGTCCCGCTGAGAGCCCGGCTCCCGCACCCGCT 1920
Db 1682 GCTCTCTTGTGGCACTTACGCGCTGTCCCGCTGAGAGCCCGGCTCCCGCACCCGCT 1741
Qy 1921 GGGCCAAACCAACCAACCCAGGCTTACAGTGGGACTATATGAGCCTGAGAGCCAG 1980
Db 1742 GGGCCAAACCAACCAACCCAGGCTTACAGTGGGACTATATGAGCCTGAGAGCCAG 1801
Qy 1981 GGGCCCCGCTGTGCCCCCACTCCCGACAAACGCTCCCGCATATATGCCGAGCTGACA 2040
Db 1802 GGGCCCCGCTGTGCCCCCACTCCCGACAAACGCTCCCGCATATATGCCGAGCTGACA 1861
Qy 2041 TTGTTACCTTGCAGGAGCGTGCACCGGGGGGACACCTATGCTGTGCTGTGACCTCCCGCAG 2100
Db 1862 TTGTTACCTTGCAGGAGCGTGCACCGGGGGGACACCTATGCTGTGCTGTGACCTCCCGCAG 1921
Qy 2101 GGGCAGTGGGGATGGGCCCCCGACAGTGAATTTCCCTGATCTGCAGTCCGCTTCAAG 2160
Db 1922 GGGCAGTGGGGATGGGCCCCCGACAGTGAATTTCCCTGATCTGCAGTCCGCTTCAAG 1981
Qy 2161 AGAAGCTTGGGAGGGGCCAGTGTGGGAGGTGCACCTGTGTGAGTGCAGAGCCCTCAAG 2220
Db 1982 AGAAGCTTGGGAGGGGCCAGTGTGGGAGGTGCACCTGTGTGAGTGCAGAGCCCTCAAG 2041
Qy 2221 ATCTGCTAGTCTTATTTCCCTTAATGTGCTGAAGGAGACCCCTTGTGTGTGAG 2280
Db 2042 ATCTGCTAGTCTTATTTCCCTTAATGTGCTGAAGGAGACCCCTTGTGTGTGAG 2101
Qy 2281 TCAGATCTTACGGCCAGATGCCACCAAGATGCCAGCTTCTCTTCCAGGAATG 2340
Db 2102 TCAGATCTTACGGCCAGATGCCACCAAGATGCCAGCTTCTCTTCCAGGAATG 2143
Qy 2341 ATTCCCTGAAGAGGTGAAGATCATGTGAGGCTCAAGGACCCCAACATCTTCCGCTGC 2400
Db 2144 ATTCCCTGAAGAGGTGAAGATCATGTGAGGCTCAAGGACCCCAACATCTTCCGCTGC 2203
Qy 2401 TGGGCGTGTGTGTCAGAGACACCCCTCTGCTGATGATTACTGACATCAATGGAAGCGGG 2460
Db 2204 TGGGCGTGTGTGTCAGAGACACCCCTCTGCTGATGATTACTGACATCAATGGAAGCGGG 2263
Qy 2461 ACCTCAACCACTTCTCTAGTCCCAACAGCTGAGAGACAGGACCGAGGGGCCCCCTG 2520
Db 2264 ACCTCAACCACTTCTCTAGTCCCAACAGCTGAGAGACAGGACCGAGGGGCCCCCTG 2323
Qy 2521 GGGAGCGGAGAGGTGCGGACAGGGGCCCCACATACAGTCAATGCTGTGCTGATGTGGAG 2580
Db 2324 GGGAGCGGAGAGGTGCGGACAGGGGCCCCACATACAGTCAATGCTGTGCTGATGTGGAG 2383
Qy 2581 CCCAGATCGCTCCGGGATGGGCTATCTGGCCAGCTCAATGTTGATGAGGGAGCTGG 2640
Db 2384 CCCAGATCGCTCCGGGATGGGCTATCTGGCCAGCTCAATGTTGATGAGGGAGCTGG 2443
Qy 2641 CCAAGCGGAACTGCTAGTGTGGGAAATTTACACATCAAAATGCAAGACTTGGCATGA 2700
Db 2444 CCAAGCGGAACTGCTAGTGTGGGAAATTTACACATCAAAATGCAAGACTTGGCATGA 2503
Qy 2701 GCGGGAACCTTATGCTGGGAGCTATACGCTGTGACGGGCGGCGAGTGTGCCATCC 2760
Db 2760 GCGGGAACCTTATGCTGGGAGCTATACGCTGTGACGGGCGGCGAGTGTGCCATCC 2760

Db 2504 GCGGGAACCTTATGCTGGGAGCTATACGCTGTGACGGGCGGCGAGTGTGCCATCC 2563
Qy 2761 GCTGATGAGCTGTGGAGTGCATCTCATGAGGAGATTTCAGAGTGCAGTGTGAGG 2820
Db 2564 GCTGATGAGCTGTGGAGTGCATCTCATGAGGAGATTTCAGAGTGCAGTGTGAGG 2623
Qy 2821 CCTTGGTGTGACCTTGTGGAGGTGCTGATGCTGTGTAGGGCCAGCCCTTGGGAGC 2880
Db 2624 CCTTGGTGTGACCTTGTGGAGGTGCTGATGCTGTGTAGGGCCAGCCCTTGGGAGC 2683
Qy 2881 TCACCGAGAGAGAGTGCATGAGAGAGCGGGGGAGTCTCCCGGAGACAGGCGCGAGG 2940
Db 2684 TCACCGAGAGAGAGTGCATGAGAGAGCGGGGGAGTCTCCCGGAGACAGGCGCGAGG 2743
Qy 2941 TGTACTGTCTCCGCGCGCTGCTGCCGAGGCGCTATATGAGAGTATGCTTGGTGT 3000
Db 2744 TGTACTGTCTCCGCGCGCTGCTGCCGAGGCGCTATATGAGAGTATGCTTGGTGT 2803
Qy 3001 GGAAGCGGAGTGTGAGACAGACAGCCTTTTCCAGCTGCAATCGGTTCTTGGCAGAG 3060
Db 2804 GGAAGCGGAGTGTGAGACAGACAGCCTTTTCCAGCTGCAATCGGTTCTTGGCAGAG 2863
Qy 3061 ATGCACTCAACAGAGTGTGATCAACATCCAGTGCCTCCCTCAGAGGAGTATCCAG 3120
Db 2864 ATGCACTCAACAGAGTGTGATCAACATCCAGTGCCTCCCTCAGAGGAGTATCCAG 2923
Qy 3121 GGAAGCGGAGTGTGAGACAGACAGCCTTTTCCAGCTGCAATCGGTTCTTGGCAGAG 3179
Db 2924 GGAAGCGGAGTGTGAGACAGACAGCCTTTTCCAGCTGCAATCGGTTCTTGGCAGAG 2883
Qy 3180 ACAGCCATCACCTTAATAGAGAGAGTGAATGAGATGCAAGGTGGGCTGGCCACCCAGGA 3239
Db 2984 ACAGCCATCACCTTAATAGAGAGAGTGAATGAGATGCAAGGTGGGCTGGCCACCCAGGA 3039
Qy 3240 GCTGATGCGCTTCTCTCTCTGAGACACACTATGATGCCCTTCTGTTTCTCTC 3299
Db 3040 GCTGATGCGCTTCTCTCTCTGAGACACACTATGATGCCCTTCTGTTTCTCTC 3099
Qy 3300 CTGAGAGCCCTGTGCGCCACCCAGCTGCTGTGAGTGGATCTCTCAACCCCTCTC 3359
Db 3100 CTGAGAGCCCTGTGCGCCACCCAGCTGCTGTGAGTGGATCTCTCTCAACCCCTCTC 3159
Qy 3360 TAGCCATCCCTTGGGAGAGGTGGGAGAAATATAGATATAGACATGACATGGCCAT 3419
Db 3160 TAGCCATCCCTTGGGAGAGGTGGGAGAAATATAGATATAGACATGACATGGCCAT 3219
Qy 3420 GAGAGACCTTGGGCCCCACTGAGACACATGATTCTCGAGAGATGGCTGCG -CCCCAGCT 3478
Db 3220 GAGAGACCTTGGGCCCCACTGAGACACATGATTCTCGAGAGATGGCTGCG -CCCCAGCT 3279
Qy 3479 TCTCTCTCTCTACACACTGAGACCCCACTGGCTGAGATGTGGGGGTGAGAGAGACA 3538
Db 3280 TCTCTCTCTCTACACACTGAGACCCCACTGGCTGAGATGTGGGGGTGAGAGAGACA 3339
Qy 3539 GAAAGAGAGAGAAATGTTCCCTTGGCCGCTGCTGCTGCTCTCTCACTTGGGCTCT 3598
Db 3340 GAAAGAGAGAGAAATGTTCCCTTGGCCGCTGCTGCTGCTCTCTCACTTGGGCTCT 3399
Qy 3599 TCTCTCTCTCTACCTGAAACACTGAGCTGGGGGTAGCCCGGCCCCCTGAGTCA - 3657
Db 3400 TCTCTCTCTCTACCTGAAACACTGAGCTGGGGGTAGCCCGGCCCCCTGAGTCA - 3459
Qy 3658 CCCCCACTTCCACTTGCAGTCTTGTAGCTAGAACTTCTCTAAGGCTATAGCTTCTGTG 3717
Db 3460 CCCCCACTTCCACTTGCAGTCTTGTAGCTAGAACTTCTCTAAGGCTATAGCTTCTGTG 3519
Qy 3718 GAGTAAATATGGGATTTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3777
Db 3520 GAGTAAATATGGGATTTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3579
Qy 3778 ATCTCTAGTGTAGTGCACATGATTTTCTATATCACTTGGGGTGTGACATTTTG 3837
Db 3580 ATCTCTAGTGTAGTGCACATGATTTTCTATATCACTT -GGGTTGTACATTTTG 3658
```


QY 3838 GGGGAGACAGACATTTTACACTATATATGACCTAGCTGAGCAATTTTATCC 3897
 |||||||
 Db 3639 GGGGAGACAGACATTTTACACTATATATGACCTAGCTGAGCAATTTTATCC 3698
 |||||||
 QY 3898 CCTGACACAGCAGGTATATTAAGCTTGAGTTTCCAC 3937
 |||||||
 Db 3699 CCTGACACAGCAGGTATATTAAGCTTGAGTTTCCAC 3738
 |||||||

RESULT 4
 LOCUS BC008716 3849 bp mRNA linear PRI 12-JUL-2001
 DEFINITION Homo sapiens, discoidin domain receptor family, member 1, clone
 MGC:8681 IMAGE:2964574, mRNA, complete cds.
 ACCESSION BC008716
 VERSION BC008716.1 GI:14250529
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3849)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.ncl.nih.gov
 CONTACT: MGC help desk
 EMAIL: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 CNA Library Preparation: Rubin Laboratory
 CNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@nih.gov
 Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McLooney, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantirlop, S., Thomas, P.J.,
 Tjongson, E.E., Touchman, J.W., Tsurgoun, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

FEATURES
 SOURCE
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov
 Series: IRAL Plate: 1 Row: 0 Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 403386.
 location/Qualifiers
 1..3849
 /organism="Homo sapiens"
 /db_xref="locusid:780"
 /db_xref="taxon:9606"
 /clone="MGC:8681 IMAGE:2964574"
 /issue_type="Muscle, rhabdomyosarcoma"
 /clone_lib="NIH-MGC-17"
 /lab_host="DH10B-R"
 /note="Vector: pOTB"
 343..2973
 /codon_start=1
 /product="discoidin domain receptor family, member 1"
 /protein_id="AA08716.1"
 /db_xref="GI:14250530"
 /translaton="MGPALISLLILLVASGDADKMGHPKRCRYALGMDRTIPD
 SDISASSWSSTNAHNSRLSSSDGAGCPAGSVPPKEEYQVLDQRLHLALVGT
 OGRHAGGLGKEFYSYRLRYSDGRMMGKDWGVEYISGNDPPEGVYLKDGPPMY
 ARLVREYPRADRYMSYCLRYELGCLMRDGLISYTPVQGTWTLSSAVYLNDSTYGH
 TVGGLDYGGLGQLADSVGLDPRKSGELRWMPGIDYVGHNSHSFGTYEMEFERD

LRAFOAMVHCNNHHTIGARLPGEVECFRRGPRAMAMEGEPMRHNLGNDPPRARV
 SVPGLGARVARILOCRFLPAGPWLIFSEISVSDVNNNSPALGTFPPAPWPPGPP
 TNFSLELEPQOOPVAKBESSPTALLIGCVAILILLILLITAMLRHLRRLLSKA
 ERYLEERELIYHLSVPGDTILINRPNGREPPYOEPRKPNPSPACVNGSAYSG
 DYMEPEKPGADLLPFPONSVPYHAEADIVLQVTOGNTAVPALPGAGADDPYV
 DFPERSRLRFKEKLEGOFEVHLCEVDSPODVLSDPLNRYKHGHPILVAVKILRPDA
 TKNARNDFLKEVKIMSRLKEDNIRILGVCVQDDPLKMTIDYMNENGLDNLGSOLE
 DKRAEAGPDGDAAGSPITISYPMILHVAAGIASGMRYATATNFHDLATRNCLVGEN
 FTIKIADGMSRNLXAGDYRVQORAVLPITNMAWECIMKFTTASVAFYTLIRE
 VLMCRAPQFQULDEVDIENAGEFFRQGRQVYLSRPPACPGLYELMKWMSRESE
 QRPFSOLHRLADALNTV"

BASE COUNT 715 a 1181 c 1165 g 788 t
 ORIGIN

Query Match 91.2% Score 3613.4 DB 9; Length 3849;
 Best Local Similarity 95.9% Pred. No. 0;
 Matches 3792; Conservative 0; Mismatches 31; Indels 130; Gaps 3;

QY 2 GGGCTGAGACTGGGGGTGACTGGGACCTAAGAGATCCGTGAGAGGCCCCGACAGC 61
 |||||||
 Db 24 GGCCCTGAGCGGAGCTGACAGCAGCCCTGGGGCCAGCTTTGAGAGCCCCGACAGC 83
 |||||||
 QY 62 TGTCTCGGAGCCGCTCCGACACCCGAGCCCGCGGCTCCCGCTCCGCGCTCC 121
 |||||||
 Db 84 TGTCTCGGAGCCGCTCCGACACCCGAGCCCGCGGCTCCCGCTCCGCGCTCC 143
 |||||||
 QY 122 CGGCTCTCGGCTCCCTCCGCGCTCCCGCGCTCCCGCGCTCCCGCGCTCC 181
 |||||||
 Db 144 CGGCTCTCGGCTCCCTCCGCGCTCCCGCGCTCCCGCGCTCCCGCGCTCC 203
 |||||||
 QY 182 CCGGCTCGAGCGCTGGGTGTGCGGGAAGAGCATGAGAGTGTCTGAAGTGTGCTATT 241
 |||||||
 Db 204 CCGGCTCGAGCGCTGGGTGTGCGGGAAGAGCATGAGAGTGTCTGAAGTGTGCTATT 263
 |||||||
 QY 242 CACTGACGATGGGGTGTGACTTGAAGATGCCAAGATGCTGCCACCCCTTAG 301
 |||||||
 Db 264 CACTGACGATGGGGTGTGACTTGAAGATGCCAAGATGCTGCCACCCCTTAG 323
 |||||||
 QY 302 GCCGAGGATCAGAGAGTATGGGACAGAGCCCTGTCATCTTACTGCTGCTCTT 361
 |||||||
 Db 324 GCCGAGGATCAGAGAGTATGGGACAGAGCCCTGTCATCTTACTGCTGCTCTT 383
 |||||||
 QY 362 GGTGCAAGTGAAGTGTGATGATGAAGAGCATTTTATCTCGCAAGTGGCGGTATGC 421
 |||||||
 Db 384 GGTGCAAGTGAAGTGTGATGATGAAGAGCATTTTATCTCGCAAGTGGCGGTATGC 443
 |||||||
 QY 422 CTTGGGATGAGAGCGGACCATCCAGACAGTACATCTCTGCTCAAGTCTCTGTC 481
 |||||||
 Db 444 CTTGGGATGAGAGCGGACCATCCAGACAGTACATCTCTGCTCAAGTCTCTGTC 503
 |||||||
 QY 482 AGATTCCACTCCCGCCCGCCAGCAGAGTGTGAAGAGCATGAGGGGATGGGCTGTG 541
 |||||||
 Db 504 AGATTCCACTCCCGCCCGCCAGCAGAGTGTGAAGAGCATGAGGGGATGGGCTGTG 563
 |||||||
 QY 542 CCCCAGAGGCTGGTGTGTTCCAGAGAGAGAGTGTGAGGTGATCTACACGACT 601
 |||||||
 Db 564 CCCCAGAGGCTGGTGTGTTCCAGAGAGAGAGTGTGAGGTGATCTACACGACT 623
 |||||||
 QY 602 CCACCTGCTGCTGTGTGGGACCCAGAGAGCGGATCGGGGGCTTGGCCAGAGACT 661
 |||||||
 Db 624 GCACCTGCTGCTGTGTGGGACCCAGAGAGCGGATCGGGGGCTTGGCCAGAGACT 683
 |||||||
 QY 662 CTCCGAGCTACCGGCTGCTGCTCCCGGATGAGTGGCGGCTGGAGGCTGGAGAGA 721
 |||||||
 Db 684 CTCCGAGCTACCGGCTGCTGCTCCCGGATGAGTGGCGGCTGGAGGCTGGAGAGA 743
 |||||||
 QY 722 CCGCTGGGCTCAGAGGTGATCTCAGGCAATGAGACCTTGAAGGAGTGTCTGAAGA 781
 |||||||
 Db 744 CCGCTGGGCTCAGAGGTGATCTCAGGCAATGAGACCTTGAAGGAGTGTCTGAAGA 803
 |||||||
 QY 782 CTTGGGCCCCCATGTTGCTGCTGCTTCAACCCCGGCTGACCGGCTCAT 841
 |||||||

Db 804 CTTGGGCCCCCAGTGGTCCGACGTGGTCCCTTACCCCGGGCTGACCGGGTCAT 863
QY 842 GAGTGTGTGTGTGGGGTAGAGCTTAATGGCTGCTGAGAGGATGAGACTGCTCTTA 901
Db 864 GAGGCTGTGTGTGGGGTAGAGCTTAATGGCTGCTGAGAGGATGAGACTGCTCTTA 923
QY 902 CACCGCCCTGTGGGGAGACAAATGATTTATCTGAGGCGGTGATCACTCAAGATCCAC 961
Db 924 CACGCCCCCTGTGGGGAGACAAATGATTTATCTGAGGCGGTGATCACTCAAGATCCAC 983
QY 962 CTATGAGGAGATACCGTGGGGGAGACAGTATGAGGAGTGGGGTCTGGCCAGGCTATGA 1021
Db 984 CTATGAGGAGATACCGTGGGGGAGACAGTATGAGGAGTGGGGTCTGGCCAGGCTATGA 1043
QY 1022 TGTGGTGGGCTGTGATGATTTAGGAAGAGTCAAGAGCTGGGGTCTGGCCAGGCTATGA 1081
Db 1044 TGTGGTGGGCTGTGATGATTTAGGAAGAGTCAAGAGCTGGGGTCTGGCCAGGCTATGA 1103
QY 1082 CTATGTGGATGAGCAACACAGCTTCTCCAGTGGCTATGTGAGATGAGATTGAGTT 1141
Db 1104 CTATGTGGATGAGCAACACAGCTTCTCCAGTGGCTATGTGAGATGAGATTGAGTT 1163
QY 1142 TGACCGGCTAGGGGCTTCCAGGCTATGAGAGTCACTGTAACAACATGCACAGCTGGG 1201
Db 1164 TGACCGGCTAGGGGCTTCCAGGCTATGAGAGTCACTGTAACAACATGCACAGCTGGG 1223
QY 1202 AGCCGCTGTGCTGGGGGGGTGGAATGTGCTTCCGGGCTGGCCATGGGCTGGGA 1261
Db 1224 AGCCGCTGTGCTGGGGGGGTGGAATGTGCTTCCGGGCTGGCCATGGGCTGGGA 1283
QY 1262 GGGGAGACCCATGCGGCACAACTAGGGGGCAACCTGGGGAGACCCAGAGCCGGGCTGT 1321
Db 1284 GGGGAGACCCATGCGGCACAACTAGGGGGCAACCTGGGGAGACCCAGAGCCGGGCTGT 1343
QY 1322 CTGAGGCCCCCTGGGGGGGCTGTGGCTGCTTCTGCAAGTCCGCTTCTTTCGGGG 1381
Db 1344 CTGAGGCCCCCTGGGGGGGCTGTGGCTGCTTCTGCAAGTCCGCTTCTTTCGGGG 1403
QY 1382 GCCCTGGTACTTCTGAGCAAAATCTCTCATCTGATGTGGTGAACAATTCCTTCC 1441
Db 1404 GCCCTGGTACTTCTGAGCAAAATCTCTCATCTGATGTGGTGAACAATTCCTTCC 1463
QY 1442 GGCAGTGGAGGACCTTCCCGCCAGCCCTGTGGGCGCTGCGCCACCTCCACCAA 1501
Db 1464 GGCAGTGGAGGACCTTCCCGCCAGCCCTGTGGGCGCTGCGCCACCTCCACCAA 1523
QY 1502 CTTTACGACCTTGTGAGAGTGGAGCCGAGAGGCGCAGAGCCCGTGGCCAAAGGCGAG 1561
Db 1524 CTTTACGACCTTGTGAGAGTGGAGCCGAGAGGCGCAGAGCCCGTGGCCAAAGGCGAG 1583
QY 1562 CCGAGACCGGATCTCATGGGGGCTGTGGGCGCATCATCTGCTGCTCATCAT 1621
Db 1584 CCGAGACCGGATCTCATGGGGGCTGTGGGCGCATCATCTGCTGCTCATCAT 1643
QY 1622 TSCCCTCATGCTGTGGCGGCTGCATGCGCAGAGGCTCTCAGCAAGGCTTAAAGGAGGT 1681
Db 1644 TSCCCTCATGCTGTGGCGGCTGCATGCGCAGAGGCTCTCAGCAAGGCTTAAAGGAGGT 1703
QY 1682 GTTGAAGAGGAGTGAAGGCTTCACTCTGTCTGCTGGGAGACATATCCTCATCAAA 1741
Db 1704 GTTGAAGAGGAGTGAAGGCTTCACTCTGTCTGCTGGGAGACATATCCTCATCAAA 1763
QY 1742 CCGCCAGGATCTTAGAGAGCAGCCCGGATACAGAGAGCCCGGCTGTGGGAATCCGCC 1801
Db 1764 CCGCCAGGATCTTAGAGAGCAGCCCGGATACAGAGAGCCCGGCTGTGGGAATCCGCC 1823
QY 1802 CCACTCCGCTTGTGTGCCCAATGAGTGTGCTGCTGCTCAATCCAGGCTAACG 1861
Db 1824 CCACTCCGCTTGTGTGCCCAATGAGTGTGCTGCTGCTCAATCCAGGCTAACG 1884
QY 1862 CCTCTTGTGGGCACTTACGCCGCTCCCTGAGAGCCCGGCGCCCAACCGGCTG 1921
Db 1885 ----- 1854
1855 ----- 1854

QY 1922 GGCCAAACCCACCAACCCAGGCTTACAGTGGGAGTATATGAGAGCTGAGAAACCAG 1981
Db 1855 ----- GCCTACAGTGGGAGTATATGAGAGCTGAGAAACCAG 1892
QY 1982 GCGCCGCTTGTGGCCGACGCTCCGACAGAGGCTCCGCCATTTAGCCGAGGCTGACAT 2041
Db 1893 GCGCCGCTTGTGGCCGACGCTCCGACAGAGGCTCCGCCATTTAGCCGAGGCTGACAT 1952
QY 2042 TGTATCCCTGAGAGGCTGACCGGGGGCAACACTATGCTGTGCTGACATGCCCCAGG 2101
Db 1953 TGTATCCCTGAGAGGCTGACCGGGGGCAACACTATGCTGTGCTGACATGCCCCAGG 2012
QY 2102 GGCAGTCCGGGATGGGCCCCCAGAGTGTATTTCCCTGATCTGCACTCCGCTTCAAGA 2161
Db 2013 GGCAGTCCGGGATGGGCCCCCAGAGTGTATTTCCCTGATCTGCACTCCGCTTCAAGA 2072
QY 2162 GAAGCTTGGAGGGGCGAGTTTGGGAGGTGACCTGTGTAGAGTCCAGACCCCTCAAGA 2221
Db 2073 GAAGCTTGGAGGGGCGAGTTTGGGAGGTGACCTGTGTAGAGTCCAGACCCCTCAAGA 2132
QY 2222 TCTGTAGTGTGATTTTCCCTTAATGTGCTTAAGGAGACCCCTTGTGTAGTGT 2281
Db 2133 TCTGTAGTGTGATTTTCCCTTAATGTGCTTAAGGAGACCCCTTGTGTAGTGT 2192
QY 2282 CAAGATCTTACGGCCAGATGCGCCACCAAGATGCCAGCTTCTCTTCTCCAGGAATGA 2341
Db 2193 CAAGATCTTACGGCCAGATGCGCCACCAAGATG-----CCAGGAATGA 2234
QY 2342 TTTCTGAAAAGGATGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTCGGCTGT 2401
Db 2235 TTTCTGAAAAGGATGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTCGGCTGT 2294
QY 2402 GGGGCTGTGTGTGAGAGACAGCCCTCTGCTGATTAATGACTACATGAGAGAGGCGA 2461
Db 2295 GGGGCTGTGTGTGAGAGACAGCCCTCTGCTGATTAATGACTACATGAGAGAGGCGA 2354
QY 2462 CCTTAACCATGTTCTCTAGTGGCCACACAGCTGAGAGACAGGCGAGGGGGCCCTGG 2521
Db 2355 CCTTAACCATGTTCTCTAGTGGCCACACAGCTGAGAGACAGGCGAGGGGGCCCTGG 2414
QY 2522 GGAAGGCGAGGCTGCGAGAGGGGCGCCACCATCATGCTACCCAAATGCTGCTGATGTGGAGC 2581
Db 2415 GGAAGGCGAGGCTGCGAGAGGGGCGCCACCATCATGCTACCCAAATGCTGCTGATGTGGAGC 2474
QY 2582 CCAAGTGGCTCGGAGCTATGCGCTATGCGCACACTCACTGATGATGGGAGCTGGG 2641
Db 2475 CCAAGTGGCTCGGAGCTATGCGCTATGCGCACACTCACTGATGATGGGAGCTGGG 2534
QY 2642 CACGCGAAGTCCCTAGTTGGGGAATTTTCAACATCAAAATGCGAGACTTTGGCATGAG 2701
Db 2535 CACGCGAAGTCCCTAGTTGGGGAATTTTCAACATCAAAATGCGAGACTTTGGCATGAG 2594
QY 2702 CCGGAACCTTATGCTGGGAGACTTACCTGTGACAGGCGCGGAGTGTGCCATCG 2761
Db 2595 CCGGAACCTTATGCTGGGAGACTTACCTGTGACAGGCGCGGAGTGTGCCATCG 2654
QY 2762 CTGAGTGGCTGGGAGAGTACCTCATGAGGGAATTCAGAGCTGGGAGTGAAGTGGGG 2821
Db 2655 CTGAGTGGCTGGGAGAGTACCTCATGAGGGAATTCAGAGCTGGGAGTGAAGTGGGG 2714
QY 2822 CTTTGTGTGACCTGTGGAGGTGTGATGCTGTAGAGGCGCCAGCCCTTGGGAGGT 2881
Db 2715 CTTTGTGTGACCTGTGGAGGTGTGATGCTGTAGAGGCGCCAGCCCTTGGGAGGT 2774
QY 2882 CACCGAGAGAGAGTATGAGAAACCGGGGAGATTCTTCGGGAGCACAGGCGCGAGGT 2941
Db 2775 CACCGAGAGAGAGTATGAGAAACCGGGGAGATTCTTCGGGAGCACAGGCGCGAGGT 2834
QY 2942 GTACCTGTCCCGGCGCTGCGGCGAGGAGGCTATATGAGCTGATGCTTGGGCGG 3001
Db 2835 GTACCTGTCCCGGCGCTGCGGCGAGGAGGCTATATGAGCTGATGCTTGGGCGG 2894

```

OY 3002 GAGCGGGAGTGTGACGACGACGACCCCTTTCCAGCTGATCGGTTCTCGGACAGAGA 3061
    |||
DB 2895 GAGCCGGAGTGTGACGACGACGACCCCTTTCCAGCTGATCGGTTCTCGGACAGAGA 2954
    |||
OY 3062 TGACCTAACACGGGTGTGATACACATTCACCTGCCCCCTCCCTAGGGAGTGTACAG 3121
    |||
DB 2955 TGACCTAACACGGGTGTGATACACATTCACCTGCCCCCTCCCTAGGGAGTGTACAG 3014
    |||
OY 3122 GGAAGCAGTGTGACCTAAACAGAGACACATGAGCCTGCCCCCTCCCTCCGAG 3181
    |||
DB 3015 GGAAGCAGTGTGACCTAAACAGAGACACATGAGCCTGCCCCCTCCCTCCGAG 3074
    |||
OY 3182 AGCCATCATCTTAATAGAGCAGTGTGATGAGTGGGCTGGGCCACCCAGGAGAC 3241
    |||
DB 3075 AGCCATCATCTTAATAGAGCAGTGTGATGAGTGGGCTGGGCCACCCAGGAGAC 3134
    |||
OY 3242 TGATGCCCCCTTCCCTTCTGTGACACCTCATGTCCCTTCTGTCTTCTCTCT 3301
    |||
DB 3135 TGATGCCCCCTTCCCTTCTGTGACACCTCATGTCCCTTCTGTCTTCTCTCT 3194
    |||
OY 3302 AGAAGCCCTGTGCCCCCAGCAGTGTGATGAGTGGGCTGGGCCACCCAGGAGAC 3361
    |||
DB 3195 AGAAGCCCTGTGCCCCCAGCAGTGTGATGAGTGGGCTGGGCCACCCAGGAGAC 3254
    |||
OY 3362 GGCATCCCTTGGGAGAGGTGGGAGAAATATAGATAGACACTGTGACATGGCCATTGG 3421
    |||
DB 3255 GGCATCCCTTGGGAGAGGTGGGAGAAATATAGATAGACACTGTGACATGGCCATTGG 3314
    |||
OY 3422 AGCACCCTGGGCCCACTGTGACAACTGATCTCTGGAGAGTGGGCTGGG - CCCCAGCTTC 3480
    |||
DB 3315 AGCACCCTGGGCCCACTGTGACAACTGATCTCTGGAGAGTGGGCTGGG - CCCCAGCTTC 3374
    |||
OY 3481 TCTCTCCCTGTGACACACTGTGACCCCACTGAGTGTGAGGAGTGTGAGAGAGACA 3540
    |||
DB 3375 TCTCTCCCTGTGACACACTGTGACCCCACTGAGTGTGAGGAGTGTGAGAGAGACA 3434
    |||
OY 3541 AGGAGAGGAAATGTTTCTTGTGCTGCTCTGTACTGTCTCTAGCTTGGGCTTCTTC 3600
    |||
DB 3435 AGGAGAGGAAATGTTTCTTGTGCTGCTCTGTACTGTCTCTAGCTTGGGCTTCTTC 3494
    |||
OY 3601 CTCCTCATCATCTGAAACACTGTGACCTGGGAGTGGGCCGCCAGCCCTAGTCACCC 3660
    |||
DB 3495 CTCCTCATCATCTGAAACACTGTGACCTGGGAGTGGGCCGCCAGCCCTAGTCACCC 3554
    |||
OY 3661 CCACCTCCCACTGTGACCTGTGTAGCTAGAACCTTCTTAAGCCTTATACGTTTCTGTGAG 3720
    |||
DB 3555 CCACCTCCCACTGTGACCTGTGTAGCTAGAACCTTCTTAAGCCTTATACGTTTCTGTGAG 3614
    |||
OY 3721 TAAATATTGGGATTTGGGGGAGAGAGGAGCAAGCCCATAGCCTTGGGGTTGACATC 3780
    |||
DB 3615 TAAATATTGGGATTTGGGGGAGAGAGGAGCAAGCCCATAGCCTTGGGGTTGACATC 3674
    |||
OY 3781 TCTAGTGTGATGACCATGATTTTCTTAATATCATCTGGGGTTTGTACATTTTGGG 3840
    |||
DB 3675 TCTAGTGTGATGACCATGATTTTCTTAATATCATCTGGGGTTTGTACATTTTGGG 3734
    |||
OY 3841 GGAGAGACACAGATTTTACATTAATATATGAGCACTAGGCAATTTTATCCCT 3900
    |||
DB 3735 GGAGAGACACAGATTTTACATTAATATATGAGCACTAGGCAATTTTATCCCT 3794
    |||
OY 3901 GGAGAGAGGATTAATTAAGCTGAGTTTCCACAAAAA 3953
    |||
DB 3795 GGAGAGAGGATTAATTAAGCTGAGTTTCCACAAAAA 3847
    |||

```

RESULT 5

```

LOCUS BC013400 3849 bp mRNA linear PRI 04-SEP-2001
DEFINITION Homo sapiens, clone MGC:3909 IMAGE:2964574, mRNA, complete cds.
ACCESSION BC013400
VERSION BC013400.1 GI:15426562
KEYWORDS MGC.
SOURCE human.

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3849)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dikhoof, Jessica Fahay, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan

FEATURES
source
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAL Plate: 10 Row: f Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 403386.
Location/Qualifiers
1..3849
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:3909 IMAGE:2964574"
/tissue_type="Muscle, Rhabdomyosarcoma"
/clone_id="N1H_MGC_17"
/lab_host="DH10B-R"
/note="vector: pOTB7"
343..2973
/codon_start=1
/product="Unknown (protein for MGC:3909)"
/protein_id="AAH13400.1"
/db_xref="gi:15426563"
/translation="MGPRALSSLLLLLVASGDADMKHFPACRYALHMODRIIPD
SDISASSWSSTARHSRLSSDDGAWCPAGSVFPEEETLOYDLDRLHVALVT
QGRHAGGGLKEFSRSLRYSRDGRMMGMDRWQOEYISGNEDEGVLLDGPVY
ARLVRFYPRADRVSVCLRLVGLGCLMDGLSLYAPVGQNYLSEAYLNDSTDG
TVGLGYGGLGOLDVYGLDPRKSOELRWPGDYGMSNHSFSSGVVEFEEDR
LRAFOAMVHONNHTTGARLPGVCECFRRGPAMAMGEMRHNLGNTDPRARAY
SVPLGRRARFLQCRFLRFGFWLFSFISITSDVYVNSPALGTFPPAPWPPPP
TNFSLELEPRGQOPVAAEESPAILIGLVAIILLILLITALLMLRHLHRLLSKA
ERRVLEELIVLHLSVPGDTILINNPPGRRPPOEPBRGNPPSACVNGSVASG
DYMEPRKGAFLPPLPPONSVPVHAEADIVLQVGTGNTAVPALPGAVGDPVR
DEPRSRLEFKELRGGEVHLEVDSPDLVSDPFLNVRKGPLVAVKILIRPDA
TKNARNDLKFKTKMSRLKDNITRLGCVQDDPDCMTTDMYEMGDLDNOLISAPLE
DKAEBAGRDQDAAGPTISPLMLHVAQAOLASGRYATATNPFVHRLDTRNCLGEN
FTITADFGMSRNLVAGDYIVVOGNAVLPIWMAMECTLMKFTASDVMAFGVTLWE
VLMCRAPQFQGLTDEQVYENAGAEFFRDGROYLSRPPACPOGLYELMLRWSRESL
ORPFSQHLRLAEDALNTV"

CDS

BASE COUNT 715 a 1181 c 1165 g 788 t
ORIGIN

Query Match 91.2%; Score 3613.4; DB 9; Length 3849;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 3792; Conservative 0; Mismatches 31; Indels 130; Gaps 3;

```

OY 2 GGGCTGAGAGCTGGGGTGTGACGACCTAAGAAATCTGACCTGAGGCCCCCAGCAGC 61
    |||
DB 24 GGGCTGAGAGCTGGGGTGTGACGACGACCCCTGGGGGCGAGCTTTGAGAGCCCCCAGCAGC 83
    |||
OY 62 TGCTCTGGGAGCGCCCTCCGACACCGGAGCCCGCGGGGCGTCCGCGTCCGCGCTCC 121
    |||
DB 84 TGCTCTGGGAGCGCCCTCCGACACCGGAGCCCGCGGGGCGTCCGCGTCCGCGCTCC 143
    |||

```

QY	122	CGGCTCTGGCTCCCTCCGCTCCCGGCGCCCTCGCCCGCCCGCGGAAGAGCCCGCTC	181
Db	144	CGGCTCTGGCTCCCTCCGCTCCCGGCGCCCTCGCCCGCGCGGAAGAGCCCGCTC	203
QY	182	CCGGGTGAGAGCGCTGGGTCTCGCCGGAAGAGCAGATGAGAGGTGCTGAAGTGGCAT	241
Db	204	CCGGGTGAGAGCGCTGGGTCTCGCCGGAAGAGCAGATGAGAGGTGCTGAAGTGGCAT	263
QY	242	CACGTAGCGATGGGGTTGGACTTTGAAGAAATGCCAAGAGATGTCGCCCCACCCCTTAG	301
Db	264	CACGTAGCGATGGGGTTGGACTTTGAAGAAATGCCAAGAGATGTCGCCCCACCCCTTAG	323
QY	302	GCCCGAGGGATCAGAGAGCTATGAGACACAGAGGCCCTGTCACTCTTACTGCTGCTCTT	361
Db	324	GCCCGAGGGATCAGAGAGCTATGAGACACAGAGGCCCTGTCACTCTTACTGCTGCTCTT	383
QY	362	GGTGGAGAAGTGGAGATGCTGACATTAAGAGGACATTTTATCTCTGCCAAGTGGCGCTATGC	421
Db	384	GGTGGAGAAGTGGAGATGCTGACATTAAGAGGACATTTTATCTCTGCCAAGTGGCGCTATGC	443
QY	422	CTTGGGCATGACAGAGCCGAGACATCCAGACAGTACATCTCTTCCACGTCCTGCTGCT	481
Db	444	CTTGGGCATGACAGAGCCGAGACATCCAGACAGTACATCTCTTCCACGTCCTGCTGCT	503
QY	482	AGATTCCATGCGCCCGCCGACACAGCTTGAAGACATGACCGGGATGGGGCTGTGTG	541
Db	504	AGATTCCATGCGCCCGCCGACACAGCTTGAAGACATGACCGGGATGGGGCTGTGTG	563
QY	542	CCCCGAGAGGTGGTGTTCCTCCAAAGAGAGAGATCTCTCAGGTGATATTAACAGACT	601
Db	564	CCCCGAGAGGTGGTGTTCCTCCAAAGAGAGAGATCTCTCAGGTGATATTAACAGACT	623
QY	602	CCACCTGTGCTGTGTGGGACCCACAGAGCAGCATGCCGGGGCCTGGGGCAAGAGATT	661
Db	624	CCACCTGTGCTGTGTGGGACCCACAGAGCAGCATGCCGGGGCCTGGGGCAAGAGATT	683
QY	662	CTCCGGAGACTACGGGGGCGCTTACTCCCGGGAGATGTCGCCGCTGGATGGGCTGAAGA	721
Db	684	CTCCGGAGACTACGGGGGCGCTTACTCCCGGGAGATGTCGCCGCTGGATGGGCTGAAGA	743
QY	722	CCGCTGGGGTCAAGAGTGTATCTCAGGCATTAAGAGACCTGAGAGGATGGTGTGAAGA	781
Db	744	CCGCTGGGGTCAAGAGTGTATCTCAGGCATTAAGAGACCTGAGAGGATGGTGTGAAGA	803
QY	782	CCTTGGGCCCCCATGTTGCCGCACTGTTCGCTCTTACCCCCGGGCTGACCGGGTCA	841
Db	804	CCTTGGGCCCCCATGTTGCCGCACTGTTCGCTCTTACCCCCGGGCTGACCGGGTCA	863
QY	842	GAGTGTCTGTGGGGGGTGAAGCTATATGAGTCTGCTCTGAGAGGATGACTCCTGTCTTA	901
Db	864	GAGTGTCTGTGGGGGGTGAAGCTATATGAGTCTGCTCTGAGAGGATGACTCCTGTCTTA	923
QY	902	CACCGCCCCCTGTGGGGCAGACAATATATATATGAGCGGTATCTACCAAGACCTCAC	961
Db	924	CACCGCCCCCTGTGGGGCAGACAATATATATGAGCGGTATCTACCAAGACCTCAC	983
QY	962	CTATACCGGAATACCGTGGGCGGACTGCAATATGAGGGGTCTGGGCGACCTGGCAGATG	1021
Db	984	CTATACCGGAATACCGTGGGCGGACTGCAATATGAGGGGTCTGGGCGACCTGGCAGATG	1043
QY	1022	TGTGGTGGGGTGGATATGATTTGAAGAAATCAGAGAGTCCGGGCTGTGGCCAGGCTATGA	1081
Db	1044	TGTGGTGGGGTGGATATGATTTGAAGAAATCAGAGAGTCCGGGCTGTGGCCAGGCTATGA	1103
QY	1082	CTATGTGGAGTGAAGACAACACAGCTTCTCAATGAGCTATGTGAGATGGAATTTGAATT	1141
Db	1104	CTATGTGGAGTGAAGACAACACAGCTTCTCAATGAGCTATGTGAGATGGAATTTGAATT	1163
QY	1142	TGACCGGCTAGAGGCTTCCAGGCTATGCAAGCTTCAACTTAACAATGACACACGCTGG	1201
Db	1164	TGACCGGCTAGAGGCTTCCAGGCTATGCAAGCTTCAACTTAACAATGACACACGCTGG	1223
QY	1202	AGCCGCTCTGCTTGGCGGGGTGAAGATGTGCGCTTCCGGGCTGGCCCTGGCAATGGCTTGGGA	1261

Db	1224	AGCCGCTGCGCCTGGGGGGTGGAAATGTCGCTCCGCGTGGCCCTGBCATGGCCTGGGA	1285
QY	1262	GGGGGAGCCCATGCGCCACAACTGAGGGGGGAACTGGGGGAGCCGAGAGCCGGGGCTGT	1321
Db	1284	GGGGGGAGCCCATGCGCCACAACTGAGGGGGGAACTGGGGGAGCCGAGAGCCGGGGCTGT	1344
QY	1322	CTGAGTGGCCCTTGGGGGGCGGTGTGGCTCGCTTTCTGCAAGTGGCCGCTCTCTTTGGGG	1381
Db	1344	CTGAGTGGCCCTTGGGGGGCGGTGTGGCTCGCTTTCTGCAAGTGGCCGCTCTCTTTGGGG	1403
QY	1382	GGCCCTGGTACTCTTCAGAGAAATGCTCTTATGTCGATGTGTGTAAATAATTCTCTCC	1443
Db	1404	GGCCCTGGTACTCTTCAGAGAAATGCTCTTATGTCGATGTGTGTAAATAATTCTCTCC	1463
QY	1442	GGGACTGGGAGGACACTTCCGCGCAGCCCGCTGTGGCGCGCTGTGGCCACACTCCACAA	1500
Db	1464	GGGACTGGGAGGACACTTCCGCGCAGCCCGCTGTGGCGCGCTGTGGCCACACTCCACAA	1522
QY	1502	CTTCAGACACTTGGAGCTGTGAGCCGAGAGGCGACAGCCCGGTGGCCAGAGCGGAGGGAG	1561
Db	1524	CTTCAGACACTTGGAGCTGTGAGCCGAGAGGCGACAGCCCGGTGGCCAGAGCGGAGGGAG	1583
QY	1562	CCGAGACCGGCATGCMCATGGGCTGCTGTGTGGCCATATATCTCTCTCTCTCATCAT	1621
Db	1584	CCGAGACCGGCATGCMCATGGGCTGCTGTGTGGCCATATATCTCTCTCTCTCATCAT	1643
QY	1622	TGCGCCATGCTCTTGGCGGTGACACTGGGCGAGGCTCTCAGAGAGGCTGAAGGAGAGGT	1681
Db	1644	TGCGCCATGCTCTTGGCGGTGACACTGGGCGAGGCTCTCAGAGAGGCTGAAGGAGAGGT	1703
QY	1682	GTTTGAAGAAGAGCTGACAGGTTTCACTCTCTGTCCCTGGGAGACATATCCTATCAAA	1741
Db	1704	GTTTGAAGAAGAGCTGACAGGTTTCACTCTCTGTCCCGGGAGACATATCCTATCAAA	1763
QY	1742	CGGCCAGGCTCCTAGAGAGGCAACCCCGGTATCAAGAGCCCGGCTCTGTGGGAATCCGCC	1801
Db	1764	CGGCCAGGCTCCTAGAGAGGCAACCCCGGTATCAAGAGCCCGGCTCTGTGGGAATCCGCC	1823
QY	1802	CGACTCGGCTCCCTGTGTGCCCAATGGCTCTGGTGTGCTCTCCAACTAGCCTACG	1861
Db	1824	CGACTCGGCTCCCTGTGTGCCCAATGGCTCTGGTGTGCTCTCCAACTAGCCTACG	1884
QY	1862	CCTCTTGTGGCACTTACGCGCGTCCCTCTGAGGCGCGGGCCCGCCACACCGCGCTG	1921
Db	1885	-----	1854
QY	1922	GGCCAAACCAACAAACAGGCTTATGAGAGCTATATGAGAGCTGAGAGGCAAG	1961
Db	1855	-----GCTTATCACTGGGGACTTATATGAGAGCTGAGAGGCAAG	1892
QY	1982	CGCCCGCTTCTGCCCCCACCCTCCGAGAAACAGCGGCCCACTTATATGCGAGGCTGACAT	2041
Db	1893	CGCCCGCTTCTGCCCCCACCCTCCGAGAAACAGCGGCCCACTTATATGCGAGGCTGACAT	1952
QY	2042	TGTTTACCTGCAAGGCGCTACACGGGGGCAACACTATGCTGTGCTGCACTGCCCCAGG	2101
Db	1953	TGTTTACCTGCAAGGCGCTACACGGGGGCAACACTATGCTGTGCTGCACTGCCCCAGG	2012
QY	2102	GGCAGTGGGGGATGGGGCCCCCGAGATGTGATTTCCCTGATGTGACATTCGCTTCAAGA	2161
Db	2013	GGCAGTGGGGGATGGGGCCCCCGAGATGTGATTTCCCTGATGTGACATTCGCTTCAAGA	2072
QY	2162	GAACTTGGGAGGCACTTTTGGGAGGTGACACTGTGTGAGTGCAGACAGCCCTCAGA	2221
Db	2073	GAACTTGGGAGGCACTTTTGGGAGGTGACACTGTGTGAGTGCAGACAGCCCTCAGA	2132
QY	2222	TCTGGTGAAGTCTGATTTCCCTTATATGTGTGCTAAGGAGACACCTTGTCTGTAGTGT	2281
Db	2133	TCTGGTGAAGTCTGATTTCCCTTATATGTGTGCTAAGGAGACACCTTGTCTGTAGTGT	2192
QY	2282	CAATCTTATGGGCGAGATGCCAAAGAAATCCAGCTTCTCTTGTTCAGAGAAATGA	2341

D	b	2193	CAGAGTCTTACGGCCAGATGCGACCAAGAAATG-----CCAGGAATGA	2235
Q	y	2342	TTTCTGAAAGAGTGAAGATCATGTGAGAGCTCAAGAGACCCCAACATCATTTGGCTGCT	2401
D	b	2235	TTTCTGAAAGAGTGAAGATCATGTGAGAGCTCAAGAGACCCCAACATCATTTGGCTGCT	2294
Q	y	2402	GGGCGTGTGTGAGAGACGACACCCCTCTGCATGATTTACTGTACTCATGAGAAAGGGGA	2461
D	b	2235	GGCGTGTGTGTGAGAGACGACACCCCTCTGCATGATTTACTGTACTCATGAGAAAGGGGA	2354
Q	y	2462	CCTCAACCAAGTTCTCTAGTGCCTCCACGACGTGAGAGCAAGGAGCGGAGGGGGCCCTG	2521
D	b	2355	CCTCAACCAAGTTCTCTAGTGCCTCCACGACGTGAGAGCAAGGAGCGGAGGGGGCCCTG	2414
Q	y	2522	GGAGGGGACGGCTCTGCGAGGGGCCACACATCAGCTACCCAAATGCTGTGATGTGGACG	2581
D	b	2415	GGAGGGGACGGCTCTGCGAGGGGGCCACACATCAGCTACCCAAATGCTGTGATGTGGACG	2474
Q	y	2582	CCAGTGGCCCTCGGGGATGGGCAATCGGCGACACACTTGTACATCGGAGACTGGC	2641
D	b	2475	CCAGTGGCCCTCGGGGATGGGCAATCGGCGACACACTTGTACATCGGAGACTGGC	2534
Q	y	2642	CACGCGGAAGTCCCTACTTGTGGGAAATTTTCACATCAAAATCGAGACTTTGGCATAG	2701
D	b	2535	CACGCGGAAGTCCCTACTTGTGGGAAATTTTCACATCAAAATCGAGACTTTGGCATAG	2594
Q	y	2702	CCGGAACCTCTATGTGTGGGACTATTACCGTGTGACGGGCGCGGACGTGTCCCATCG	2761
D	b	2595	CCGGAACCTCTATGTGTGGGACTATTACCGTGTGACGGGCGCGGACGTGTCCCATCG	2654
Q	y	2762	CTGAGTGGCCCTGGGAGAGCAATCCTCAATGGGAAAGTTCACAGATGGGATGAGCTGGGC	2821
D	b	2655	CTGAGTGGCCCTGGGAGAGCAATCCTCAATGGGAAAGTTCACAGATGGGATGAGCTGGGC	2714
Q	y	2822	CTTTGTGTGACCTGTGGGAGGTGTGTGATGTCTGTAGGGGCCACGCTTTGGGCACT	2881
D	b	2715	CTTTGTGTGACCTGTGGGAGGTGTGTGATGTCTGTAGGGGCCACGCTTTGGGCACT	2774
Q	y	2882	CACCGAGAGCAGGATCTACGAGAACGCGGGGGAGTTCTTCCGGGACACGAGCGCGGACGT	2941
D	b	2775	CACCGAGAGCAGGATCTACGAGAACGCGGGGGAGTTCTTCCGGGACACGAGCGCGGACGT	2834
Q	y	2942	GTACCTTCCCCGCGCTGTGCTGCTGCGCCGAGGGCCATATGAGCTGATGCTTCGGTGTG	3001
D	b	2835	GTACCTTCCCCGCGCTGTGCTGCTGCGCCGAGGGCCATATGAGCTGATGCTTCGGTGTG	2894
Q	y	3002	GAGCGGGAGTGTGAGAGCAGACACCTTTTCCAGCTGCATGCGTTCGAGGAGAGGA	3061
D	b	2895	GAGCGGGAGTGTGAGAGCAGACACCTTTTCCAGCTGCATGCGTTCGAGGAGAGGA	2954
Q	y	3062	TGCACCTACACAGGTGTGAATTCACATCAGCTGACGCTCCCTCCAGGAGTGAATCCAG	3121
D	b	2955	TGCACCTACACAGGTGTGAATTCACATCAGCTGACGCTCCCTCCAGGAGTGAATCCAG	3014
Q	y	3122	GGAAGCCAGTGAACATTAATAAGAGAGACAAATGGACCTTGTGCTTCCCTCCGAC	3181
D	b	3015	GGAAGCCAGTGAACATTAATAAGAGAGACAAATGGACCTTGTGCTTCCCTCCGAC	3074
Q	y	3182	AGCCCATCACCTCTAATATAGAGGCAATGACACTGCAAGTGGGGCCACCCAGGGAGC	3241
D	b	3075	AGCCCATCACCTCTAATATAGAGGCAATGACACTGCAAGTGGGGCCACCCAGGGAGC	3134
Q	y	3242	TGATGCCCTTCTCCCTTCTGTGACACACTTCATGTGCCCTTCTGTTCCTTCTCT	3301
D	b	3135	TGATGCCCTTCTCCCTTCTGTGACACACTTCATGTGCCCTTCTGTTCCTTCTCT	3194
Q	y	3302	AGAAAGCCCTGTGCGCCACCCAGCTGTGCTGTGATGGGATCTCTCCACCTCTCTA	3361
D	b	3195	AGAAAGCCCTGTGCGCCACCCAGCTGTGCTGTGATGGGATCTCTCCACCTCTCTA	3254
Q	y	3362	GCCATCCCTTGGGAAAGGGGGGGAATATAGATGAGACATGAGATGGCCCATTTGG	3421
D	b	3255	GCCATCCCTTGGGAAAGGGGGGGAATATAGATGAGACATGAGATGGCCCATTTGG	3314

QY	3422	AGCACCCTGGGCCCCCACTGGACAACAAC	TAGTTCCTGTGGAGAGTGGCGG-CCCAAGCTTC	3480
Db	3315	AGCACCCTGGGCCCCCACTGGACAACAAC	TAGTTCCTGTGGAGAGTGGCGGCCCCCAAGCTTC	3374
QY	3481	TCTCTCCCTGTGCACA	CACTGGACCCCACTGGCTGAGAAATCTGGGGGTGAGAGACAA	3540
Db	3375	TCTCTCCCTGTGCACA	CACTGGACCCCACTGGCTGAGAAATCTGGGGGTGAGAGACAA	3434
QY	3541	AGGAGAGGAAATGATTCTCTGTGGCTGTGCTGTG	ACTGTCTCAGACTTGGGACTTCCTC	3600
Db	3435	AGGAGAGGAAATGATTCTCTGTGGCTGTGCTGTG	ACTGTCTCAGACTTGGGACTTCCTC	3494
QY	3601	CTCTCCATCACCCTGA	AAACACTGGACCTGGGGGTAGCCCCGCCAGCCCTCAGTCACC	3660
Db	3495	CTCTCCATCACCCTGA	AAACACTGGACCTGGGGGTAGCCCCGCCAGCCCTCAGTCACC	3554
QY	3661	CCACTTCCCACTGAGAGTCTTACTCTGAAATCTCT	CTPAAGCTTATGACTTCTGTGGAG	3720
Db	3555	CCACTTCCCACTGAGAGTCTTACTCTGAAATCTCT	CTPAAGCTTATGACTTCTGTGGAG	3614
QY	3721	TAAATATTGGAGTTGGGGGAAAGAGAGGAC	CAAGCCCATAGCCTTGGGGTGGACATC	3780
Db	3615	TAAATATTGGAGTTGGGGGAAAGAGAGGAC	CAAGCCCATAGCCTTGGGGTGGACATC	3674
QY	3781	TCTATGTAGAGCGAC	ACATGATTTTCTATATACACTGGGGGTTGTCAATTTTGGG	3840
Db	3675	TCTATGTAGAGCGAC	ACATGATTTTCTATATACACTGGGGGTTGTCAATTTTGGG	3734
QY	3841	GGAGAGACACAGATTTTACAC	TATATATGACCTAGCTTAGGCACATTTTATCCCT	3900
Db	3735	GGAGAGACACAGATTTTACAC	TATATATGACCTAGCTTAGGCACATTTTATCCCT	3794
QY	3901	GCACTAGCAGGTAATTA	TAAAGGTGATTTCCACAAAAA	3953
Db	3795	GCACTAGCAGGTAATTA	TAAAGGTGATTTCCACAAAAA	3847

	RESULT	6
HOMCAK		
LOCUS	HUMCAK	3803 bp mRNA linear PRI 11-MAY-1994
DEFINITION	Homo sapiens tyrosine protein kinase (cck) gene, complete cds.	
ACCESSION	L20817	
VERSION	L20817.1 GI:306474	
KEYWORDS	A5-antigen; factor V; factor VIII; tyrosine protein kinase.	
SOURCE	Homo sapiens fetus liver CDNA to mRNA.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3803)	
AUTHORS	Perez,J.L., Shen,X., Finkernagel,S., Scliorra,L., Jenkins,N.A., Gilbert,D.J., Copeland,N.G., and Wong,T.W.	
TITLE	Identification and chromosomal mapping of a receptor tyrosine kinase with a putative phospholipid binding sequence in its ecodomain	
JOURNAL	Oncogene 9, 211-219 (1994)	
MEDLINE	94134417	
REFERENCE	2 (bases 1 to 3803)	
AUTHORS	Johnson,J.D.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-FEB-1993) J.D. Johnson	
REFERENCE	3 (sites)	
AUTHORS	Johnson,J.D., Edman,J.C. and Ruter,W.J.	
TITLE	A receptor tyrosine kinase found in breast carcinoma cells has an extracellular discoidin I-like domain	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)	
MEDLINE	93296201	
REFERENCE	4 (sites)	
AUTHORS	Mong,T.	
TITLE	Direct Submission	
JOURNAL	Submitted (06-JUL-1993) T. Mong	
FEATURES	Location/Qualifiers	
SOURCE	I..3803	

Db	1442	CCATCCTCATGGCGTGGCTGGTGGCCATCATCTGCTCCTGCTGCTCATCTAGGCCCTCA	1501
Qy	1630	TGCTTGGCGGCTCTCACTGGCGAGGCTCCTCAGCAAGGCTCAACGAGGGTTTGAAG	1689
Db	1502	TGCTTGGCGGCTCACTGGCGAGGCTCCTCAGCAAGGCTCAAGGAGGGTGTGAAG	1561
Qy	1690	AGGACCTAGGGTTCACTCTGCTGCTGGGGACCTATCTCTCAATCAAAACGCCCCAG	1749
Db	1562	AGGACCTAGCGTTCACTCTGCTGCTGGGGACCTATCTCTCAATCAAAACGCCCCAG	1621
Qy	1750	GTCTAGAGAGCCACCCCGTACAGAGAGCCCGGCTGTGGGATCGGCCCACTCG	1809
Db	1622	GTCTAGAGAGCCACCCCGTACAGAGAGCCCGGCTGTGGGATCGGCCCACTCG	1661
Qy	1810	CTCCCTGTGTCCCAATAGGCTCTGTGTGCTCTCCATCCAGCTACCGCTCTTC	1869
Db	1662	CTCCCTGTGTCCCAAGGGCTGTGCTGTGTCTCTCAATCCAGCTACCGCTCTTC	1741
Qy	1870	TGGCACTTACGGCCGTCCCTCGAGAGCCGGGGCCCCCACACCGCGTGGGCAAC	1929
Db	1742	TGGCACTTACGGCCGTCCCTCGAGAGCCGGGGCCCCCACACCGCGTGGGCAAC	1801
Qy	1930	CCACCAACACCCAGGCTACAGTGGGAGCTATATGAGCTTGAGAGCCAGCGCCCGC	1989
Db	1802	CCACCAACACCCAGGCTACAGTGGGAGCTATATGAGCTTGAGAGCCAGCGCCCGC	1861
Qy	1990	TTTCGCCCCCACTCCCCACACAGGGTCCCCATTATGCGGAGGCTACATTTGTACC	2049
Db	1862	TTTCGCCCCCACTCCCCACACAGGGTCCCCATTATGCGGAGGCTACATTTGTACC	1921
Qy	2050	TGCAGGGGCTACCGGGGGGACACCTATGCTGTGCTGACATGCCCCAGGGGACATG	2109
Db	1922	TGCAGGGGCTACCGGGGGGACACCTATGCTGTGCTGACATGCCCCAGGGGACATG	1961
Qy	2110	GGGATGGGGCCCCCAGAGTGGGATTTCCCTCGATCTCGACTCCGCTTCAAGAGAAGCTG	2169
Db	1962	GGGATGGGGCCCCCAGAGTGGGATTTCCCTCGATCTCGACTCCGCTTCAAGAGAAGCTG	2041
Qy	2170	GCGAGGGCAGTTTGGGGAGTGCACCTGTGTGAGGTGCACAGCCCTCAATCTGTGCA	2229
Db	2042	GCGAGGGCAGTTTGGGGAGTGCACCTGTGTGAGGTGCACAGCCCTCAATCTGTGCA	2101
Qy	2220	GTCCTGATTTCCCTTATGTGCGTAAGGAGACCCCTTGTGCTAGCTCAAGATCT	2289
Db	2102	GTCCTGATTTCCCTTAAGTGTCGTAAAGGAGACCCCTTGTGCTAGCTCAAGATCT	2161
Qy	2290	TACGGCAGATGCGACCAACAATGCCAGCTTCTGTTGCCAGGAATATTTCTGA	2349
Db	2162	TACGGCAGATGCGACCAACAATGCCAGCTTCTGTTGCCAGGAATATTTCTGA	2203
Qy	2350	AAGAGTGGAAGATCATGTGAGGCTCGAAGAGCCCAACATCATTTGCTGTGGGCTGT	2409
Db	2204	AAGAGTGGAAGATCATGTGAGGCTCGAAGAGCCCAACAATCATTTGCTGTGGGCTGT	2263
Qy	2410	GTCGACGAGAGACCCCTGTGATGATATTCAGTACATGAGAGAAAGCGCACTCAAC	2469
Db	2264	GTCGACGAGAGACCCCTGTGATGATATTCAGTACATGAGAGAAAGCGCACTCAAC	2323
Qy	2470	AGTTCTCAGTGGCCACACAGCTGAGAGACAAAGCAGCCGAGGGGGCCCTTGGGACGGG	2529
Db	2324	AGTTCTCAGTGGCCACACAGCTGAGAGACAAAGCAGCCGAGGGGGCCCTTGGGACGGG	2383
Qy	2530	AGGCTGGCGCAGGGGCCACCATATGCTACCCATCTGCTGATGTGGCAGCCAGATCG	2589
Db	2384	AGGCTGGCGCAGGGGCCACCATATGCTACCCATCTGCTGATGTGGCAGCCAGATCG	2443
Qy	2590	CTCTCGGCATAGCGCTATCTGGCCACACTCACTCAATTTGTACATCGGGACCTGGCCACGGGGA	2649
Db	2444	CTCTCGGCATAGCGCTATCTGGCCACACTCACTCAATTTGTACATCGGGACCTGGCCACGGGGA	2503
Qy	2650	ACTGCGTAGTTGGGGAAAAATTTACCATCAAAATGCGAGACTTTGGCATGAGCCGGAAC	2709

D	2504	ACTGCTAGTTGGGGAAAAATTTTCCACATCTCAAAATCCGACACTTTTG6CATGA6CCGGAAAC	2563
Q	2710	TCATATGCTGGGGACTATTTACCGTCGTGTGCAAGGGCCGGGGCAGATGTCGCCATCCGCTGGATGG	2765
D	2564	TCATAGCGGGGACTATTTACCGTGTGTGAGGGCCGGGGCAGTGTGCCCATCCGCTGGATGG	2623
Q	2770	CCTGGGAGTGCATCTCTATG6GGGAAAGTTCAAGCACTGCGAGTGA6GTGAGTGTGGCTTTTG6TG	2829
D	2624	CCTGGAGTGCATCTCTATG6GGGAAAGTTCAAGCACTGCGAGTGA6GTGAGTGTGGCTTTTG6TG	2683
Q	2830	TGACCCGTGTGGAGGTGCTCATGCTGTGTAGGGCCCAAGCCCTTTTGGGAGGCTCACCAGAC	2883
D	2684	TGACCCGTGTGGAGGTGCTCATGCTGTGTAGGGCCCAAGCCCTTTTGGGAGGCTCACCAGAC	2743
Q	2890	AGCAGGTATATGAAAGCGCGGGGAGTTCTCCGGGACCAAGGGCCGGCAGGTACCTGT	2949
D	2744	AGCAGGTATATGAAAGCGCGGGGAGTTCTCCGGGACCAAGGGCCGGCAGGTACCTGT	2803
Q	2950	CCGGGCGGCTGCTGCGCCGACAGGGCTATATGATAGCTGATGCTTGCTGTGAGACCGGG	3009
D	2804	CCGGGCGGCTGCTGCGCCGACAGGGCTATATGATAGCTGATGCTTGCTGTGAGACCGGG	2863
Q	3010	AGTGTAGAGACGACCAACCTTTTCCAGTGTGATGGTCTCTGGCAGAGATGCATCTCA	3058
D	2864	AGTGTAGAGACGACCAACCTTTTCCAGTGTGATGGTCTCTGGCAGAGATGCATCTCA	2923
Q	3070	ACACGGTGTGATATACATATCCAGATGCGCCCTCCCTCAGGAGTGTATCCAGGGGAAAGCA	3129
D	2924	ACACGGTGTGATATACATATCCAGATGCGCCCTCCCTCAGGAGTGTATCCAGGGGAAAGCA	2983
Q	3130	GTGACACTAAAAACAAGAGACACAAATGGCAGCTCTGTGCTCCCTCCCGAGAGCCATC	3189
D	2984	GTGACACTAAAAACAAGAGAGACAAATGGACACCTGTGCTCCCTCCCGAGAGCCATC	3043
Q	3190	ACCTCTAATAGAGCACTGAGACTGCAAGTGGGCTGTGGCCCAACCAAGGAGCTGATGCC	3249
D	3044	ACCTCTAATAGAGCACTGAGACTGCAAGTGGGCTGTGGCCCAACCAAGGAGCTGATGCC	3098
Q	3250	CTTCTCCCTCCCTCGGAGACACTCTCATGTCGCCCTTCCTGTCTTCCCTCTAGAGAGCC	3309
D	3099	CTTCTCCCTCCCTCGGAGACACTCTCATGTCGCCCTTCCTGTCTTCCCTCTAGAGAGCC	3158
Q	3310	CTGTGCGCCACCAAGCTGCTGCTGTGATGGGATGGAATCTCTCCACCCCTCTAGCCATCC	3369
D	3159	CTGTGCGCCACCAAGCTGCTGCTGTGATGGGATGGAATCTCTCCACCCCTCTAGCCATCC	3218
Q	3370	TTGGGGGAAAGGCTGGGGAGAAATATAGGATAGACACTGACATGGCCATTTGGAGCACTG	3429
D	3219	TTGGGGGAAAGGCTGGGGAGAAATATAGGATAGACACTGACATGGCCAAATTTGGAGCACTG	3278
Q	3430	GGCCCCACTGGAACAACGTATATTCGAGAGAGGTGGCTGGCCCCAGGTCGTCTCTCCCT	3489
D	3279	GGCCCCACTGGAACAACGTATATTCGAGAGAGAG-----ACCACAGCTCTCTCTCCCT	3333
Q	3490	GTCACACACTGAGACCCCACTGGCTGTGAATCTTGGGGGTGAGGAGAGACAAGAGAGAGGA	3549
D	3334	GTCACACACTGAGACCCCACTGGCTGTGAATCTTGGGGGTGAGGAGAGACAAGAGAGAGGA	3393
Q	3550	AAATGTTCTTGTGCTGCTGCTGTACTTGTCTCTAGCTTGCTTGCTTCTCTCTCAT	3609
D	3394	AAATGTTCTTGTGCTGCTGCTGTACTTGTCTCTAGCTTGCTTGCTTCTCTCTCAT	3453
Q	3610	CACCTGAAACAGAGACGTGGGGGTGAGCCGCCCAAGCCCACTAAGACCCCACTTCCC	3669
D	3454	CACCTGAAACAGAGACGTGGGGGTGAGCCGCCCAAGCCCACTAAGACCCCACTTCCC	3513
Q	3670	ACTTGCAGTCTTGTAGCTAGAACTTCTCTAACCCTATACAGTTCTGTGTAGATTAATATTTG	3729
D	3514	ACTTGCAGTCTTGTAGCTAGAACTTCTCTAACCCTATACAGTTCTGTGTAGATTAATATTTG	3571
Q	3730	GGATTTGGGGGAAAGAGGAGCAACGGGCCCATAGGCTTTGGGGTTGAGATCTTAGTGA	3789
D	3572	GGATTTGGGGGAAAGAGGAGCAACGGGCCCATAGGCTTTGGGGTTGAGATCTTAGTGA	3630

QY 3790 GCTGCCACATGATTTTCTATATATCATCTGGGGTTGTACATTTTGGGGGAGAGACA 3849
|||||
Db 3631 GGTGCCACATGATTTTCTATATATCATCTGGGGTTGTACATTTTGGGGGAGAGACA 3690
QY 3850 CAGATTTTACACTAATATATGACCTAGCTGAGCAATTTTAATCCCTGCACATAGGC 3909
|||||
Db 3691 CAGA-TTTTACACTAATATATGACCTAGCTGAGCAATTTTAAT-CCCTGCACATAGGC 3748
QY 3910 AGCTAATATAAGGTGAGTTTCCACAAAAA 3953
|||||
Db 3749 AGCTAATATAAGTTGAGTTTCCAAAAA 3792

RESULT 7
AR094160 3637 bp DNA linear PAT 08-SEP-2000
LOCUS DEFINITION Sequence 3 from patent US 6001621.
ACCESSION AR094160
VERSION AR094160.1 GI:10020905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3637)
AUTHORS Godowski, P.J., Mark, M.R. and Scadden, D.T.
TITLE Protein tyrosine kinases
JOURNAL Patent: US 6001621-A 3 14-DEC-1999;
FEATURES location/qualifiers
SOURCE 1. 3637
/organism="unknown"

BASE COUNT 721 a 1094 c 1079 g 743 t
ORIGIN

Query Match 87.1%; Score 3451; DB 6; Length 3637;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;

QY 256 GTTGACTTGAAGAAATCCAGAGATGTCGCCACCCCTTAGGCCCGAGGATCAG 315
Db 17 GTTGACTTGAAGAAATCCAGAGATGTCGCCACCCCTTAGGCCCGAGGATCAG 76
QY 316 GAGCTATGGAGCAGAGAGCCCTGTCATCTTACTGCTGCTTGGTGCAATGAG 375
Db 77 GAGCTATGGAGCAGAGAGCCCTGTCATCTTACTGCTGCTTGGTGCAATGAG 136
QY 376 ATGCTGACATGAAGGACATTTTGAATCCTCCAAAGTCCCGCTATGCCCTGGGATGACAG 435
Db 137 ATGCTGACATGAAGGACATTTTGAATCCTCCAAAGTCCCGCTATGCCCTGGGATGACAG 196
QY 436 ACCGACCATCCAGACAGTACATCTGCTCCAGCTCTGTCACATTTCCACTGCCG 495
Db 197 ACCGACCATCCAGACAGTACATCTGCTCCAGCTCTGTCACATTTCCACTGCCG 256
QY 496 CCCGCCACAGAGAGTTGAGAGACAGTACGCGGATGGGCTGTCGCCGACAGGATCGG 555
Db 257 CCCGCCACAGAGAGTTGAGAGACAGTACGCGGATGGGCTGTCGCCGACAGGATCGG 316
QY 556 TGTTTCCCAAGAGAGAGAGTACTTGACAGGTGATCTACAAAGACTCCACTGTGGCTC 615
Db 317 TGTTTCCCAAGAGAGAGAGTACTTGACAGGTGATCTACAAAGACTCCACTGTGGCTC 376
QY 616 TGGTGGACACCAAGAGAGAGTCCGGGGCTTGGGCAAGAGATTTCCCGGAGCTAC 675
Db 377 TGGTGGACACCAAGAGAGAGTCCGGGGCTTGGGCAAGAGATTTCCCGGAGCTAC 436
QY 676 GGGTGGCTTACTCCCGGAGATGTCGCGCTGATGGGCTGGAGACGCTGGGGTACG 735
Db 437 GGGTGGCTTACTCCCGGAGATGTCGCGCTGATGGGCTGGAGACGCTGGGGTACG 496
QY 736 AGTGATCTAGGCATGAGGACCTTGAAGAGTGTGTGAAGACCTTGGGCCCCCA 795
|||||

Db 497 AGTGATCTAGGCATGAGGACCTTGAAGAGTGTGTGAAGACCTTGGGCCCCCA 556
QY 796 TGGTCCCGGACTGTTGCTTCTACCCCGGGCTACCGGGGTCATGATGTCGTGTC 855
Db 557 TGGTCCCGGACTGTTGCTTCTACCCCGGGCTACCGGGGTCATGATGTCGTGTC 616
QY 856 GGGTAAAGCTATGAGCTGCTTGTGAGAGATGAGTCTGTGCTTACACCGCCCTGTGG 915
Db 617 GGGTAAAGCTATGAGCTGCTTGTGAGAGATGAGTCTGTGCTTACACCGCCCTGTGG 676
QY 916 GCGAGCAATGATTTATCTGAGGCGCTTACCTCAACAGCTCCACTATGACGACATA 975
Db 677 GCGAGCAATGATTTATCTGAGGCGCTTACCTCAACAGCTCCACTATGACGACATA 736
QY 976 CCGTGGCGGACTGCAGATGAGGAGTCTGGGCGAGCTGAGATGGTGTGGGGCTGG 1035
Db 737 CCGTGGCGGACTGCAGATGAGGAGTCTGGGCGAGCTGAGATGGTGTGGGGCTGG 796
QY 1036 ATGACTTTAGGAAGATCAGAGCTGCGGCTGCGCAGGCTATGACTATGTGGATGGA 1095
Db 797 ATGACTTTAGGAAGATCAGAGCTGCGGCTGCGCAGGCTATGACTATGTGGATGGA 856
QY 1096 GCAACACAGCTTCTCCAGTGTGCTATGTGAGATGAGATTTGATGACCGGCTGAGG 1155
Db 857 GCAACACAGCTTCTCCAGTGTGCTATGTGAGATGAGATTTGATGACCGGCTGAGG 916
QY 1156 CTTCCAGGCTATGCAAGCTGCACTGTACACATGATGATGAGAGAGAGAGAGAGAG 1215
Db 917 CTTCCAGGCTATGCAAGCTGCACTGTACACATGATGATGAGAGAGAGAGAGAGAG 976
QY 1216 GCGGGGTGGAATGCTGCTCCGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1275
Db 977 GCGGGGTGGAATGCTGCTCCGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1036
QY 1276 GCCACACCTAGAGGGGCAACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1335
Db 1037 GCCACACCTAGAGGGGCAACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1096
QY 1336 GCGGCGGTGTGCTGCTTCTGCAAGTCCCGCTTCTTGGGAGAGAGAGAGAGAGAG 1395
Db 1097 GCGGCGGTGTGCTGCTTCTGCAAGTCCCGCTTCTTGGGAGAGAGAGAGAGAGAG 1156
QY 1396 TCAGGGAATCTCTCATCTGATGTGAGTGAATTTCTCTCCGACATGGAGAGCA 1455
Db 1157 TCAGGGAATCTCTCATCTGATGTGAGTGAATTTCTCTCCGACATGGAGAGCA 1216
QY 1456 CTTCCCGGCAAGCCCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1515
Db 1217 CTTCCCGGCAAGCCCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1276
QY 1516 AGCTGAGAGCCAG 1575
Db 1277 AGCTGAGAGCCAG 1336
QY 1576 TCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1635
Db 1337 TCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1396
QY 1636 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1695
Db 1397 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1456
QY 1696 TGACGGTTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1755
Db 1457 TGACGGTTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1516
QY 1756 GAGAGCAACCCCGTACAG 1815
Db 1517 GAGAGCAACCCCGTACAG 1576
QY 1816 GTGTCCCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1875
Db 1577 GTGTCCCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1636

QY 1876 CTTAGCCCGGTCCTCCGAGGCGGCGGCCCCCACCACCGGCTGGGCAAAACCCACCA 1935
DB 1637 CTTAGCGCCGTCCTCCGAGGCGGCGGCCCCCACCACCGGCTGGGCAAAACCCACCA 1696
QY 1936 ACACCCAGGCTACAGTGGGGAGCTATATGAGCCGTGAGAAACCGAGCCGCCCTTCTGC 1995
DB 1637 ACACCCAGGCTACAGTGGGGAGCTATATGAGCCGTGAGAAACCGAGCCGCCCTTCTGC 1756
QY 1996 CCCCACCTCCCGAGAACAGCTCCCGCATTTATGCCGAGGCTGACATTTGTACCCCTGACG 2055
DB 1757 CCCCACCTCCCGAGAACAGCTCCCGCATTTATGCCGAGGCTGACATTTGTACCCCTGACG 1816
QY 2056 GCGTACCGGGGGCAACAGCTATGCTGCTGCTGACCTGCCCCCAGAGGAGTCGGGATG 2115
DB 1817 GCGTACCGGGGGCAACAGCTATGCTGCTGCTGACCTGCCCCCAGAGGAGTCGGGATG 1876
QY 2116 GGGCCCCAGAGTGGATTTCCCTGANTGCTGACCTCCGTTTAAAGAGAACTTGGCGAG 2175
DB 1877 GGGCCCCAGAGTGGATTTCCCTGANTGCTGACCTCCGTTTAAAGAGAACTTGGCGAG 1936
QY 2176 GCCAGTTGGGAGAGTGCACCTGTGTGAGTGCAGACGCTCAAGATGTGTCAGTCTG 2235
DB 1937 GCCAGTTGGGAGAGTGCACCTGTGTGAGTGCAGACGCTCAAGATGTGTCAGTCTG 1936
QY 2236 ATTTCCTCCCTTAATGTGCTGAAGGACACCTTTGCTGTGCTGCAAGATCTTACGGC 2295
DB 1937 ATTTCCTCCCTTAATGTGCTGAAGGACACCTTTGCTGTGCTGCAAGATCTTACGGC 2056
QY 2296 CAGATGCCACCAAGAAATGCCAGTTCTCTGCTCCAGAAATGATTTCTGAAAGAG 2355
DB 2057 CAGATGCCACCAAGAAATGCCAGTTCTCTGCTCCAGAAATGATTTCTGAAAGAG 2098
QY 2356 TGAAGATCATGTGAGGCTCAAGAGACCCCAACATCATTCGCTGCGCTGTGTGTC 2415
DB 2099 TGAAGATCATGTGAGGCTCAAGAGACCCCAACATCATTCGCTGCGCTGTGTGTC 2138
QY 2416 AGGACGACCCCTCTGCATGATTTACTGACTACATGAGAGAGCGGACCTCAACAGTTCC 2475
DB 2159 AGGACGACCCCTCTGCATGATTTACTGACTACATGAGAGAGCGGACCTCAACAGTTCC 2218
QY 2476 TCAGTGGCCACACGATGGAGAGCAAGGAGCGAGGGGGGCTGGGAGCGGAGAGCTG 2535
DB 2219 TCAGTGGCCACACGATGGAGAGCAAGGAGCGAGGGGGGCTGGGAGCGGAGAGCTG 2278
QY 2536 CGCAGGGGCGCCACCATGACTACCAATGCTGCTGATGTGGCAGCCAGATCCCTCGC 2595
DB 2279 CGCAGGGGCGCCACCATGACTACCAATGCTGCTGATGTGGCAGCCAGATCCCTCGC 2338
QY 2596 GCATGGCGCTATCTGGCAGACTCACTTTGTACATCGGGAGCTGGCAACCGGAACTGCC 2655
DB 2339 GCATGGCGCTATCTGGCAGACTCACTTTGTACATCGGGAGCTGGCAACCGGAACTGCC 2398
QY 2656 TAGTGGGGGAAAAATTCACCATCAAAATCGAGACTTGGCATGAGCGGAACTCATG 2715
DB 2399 TAGTGGGGGAAAAATTCACCATCAAAATCGAGACTTGGCATGAGCGGAACTCATG 2458
QY 2716 CTGGGAGCTATTACCTGTGTGAGGCGGCGGAGTGTGCCATCCGCTGAGTGGCTGG 2775
DB 2459 CTGGGAGCTATTACCTGTGTGAGGCGGCGGAGTGTGCCATCCGCTGAGTGGCTGG 2518
QY 2776 AGTGCATCTTCATGAGGAAATTACGACTGCGAGTACAGTGTGGGCTTTGGTGTGACC 2835
DB 2519 AGTGCATCTTCATGAGGAAATTACGACTGCGAGTACAGTGTGGGCTTTGGTGTGACC 2578
QY 2836 TGTGGAGGTGCTGATCTGTGTAGGGCCAGCCCTTGGGAGCTACAGGAGAGAGG 2895
DB 2579 TGTGGAGGTGCTGATCTGTGTAGGGCCAGCCCTTGGGAGCTACAGGAGAGAGG 2638
QY 2896 TCATCGAAGACGGGGGAGATTCTTCGGGAGCAAGGCGCGCAGAGTGTACCTGTCCGGC 2955
DB 2639 TCATCGAAGACGGGGGAGATTCTTCGGGAGCAAGGCGCGCAGAGTGTACCTGTCCGGC 2698

QY 2956 CGCCTGCTGCCCGGAGGCGCTATATGAGCTGATCTCGGTGTGTGAGCCGGAGTCTG 3015
DB 2699 CGCCTGCTGCCCGGAGGCGCTATATGAGCTGATCTCGGTGTGTGAGCCGGAGTCTG 2758
QY 3016 AGCAGCGACACCTTTTCCAGCTGCAATCGGTTCTTGGCAGAGAGTACTCAACAGG 3075
DB 2759 AGCAGCGACACCTTTTCCAGCTGCAATCGGTTCTTGGCAGAGAGTACTCAACAGG 2818
QY 3076 TGTGAATACATTCACACTGCTCCCTCCCTCAGAGGAGTATCCAGGGAACGATGACA 3135
DB 2819 TGTGAATACATTCACACTGCTCCCTCCCTCAGAGGAGTATCCAGGGAACGATGACA 2878
QY 3136 CTAAGCAAGAGAGACAAATGAGCACTCTGCCCTTCCCTCCCGACAGCCCATCACTCT 3195
DB 2879 CTAAGCAAGAGAGACAAATGAGCACTCTGCCCTTCCCTCCCGACAGCCCATCACTCT 2938
QY 3196 AATAGAGCAATGAGACTGCAAGTGGCTGGGCCACCCAGAGAGTATGCCCTTCTC 3255
DB 2939 AATAGAGCAATGAGACTGCAAGTGGCTGGGCCACCCAGAGAGTATGCCCTTCTC 2958
QY 3256 CCCTTCTGAGACACTCTCATGTCCCTTCTCTCTCTCTAGAGCCCTGTGCG 3315
DB 2959 CCCTTCTGAGACACTCTCATGTCCCTTCTCTCTCTCTAGAGCCCTGTGCG 2972
QY 3316 CCAACCAAGCTGTGCTGTGATGGGATCTCTCCACCTCTCTAGCCATCCCTTGGGG 3375
DB 2973 CCAACCAAGCTGTGCTGTGATGGGATCTCTCCACCTCTCTAGCCATCCCTTGGGG 3032
QY 3376 AAGGTGGGGGAAATATAGATAGACACTGGAATGGCCATTTGGACACTTGGCCCC 3435
DB 3033 AAGGTGGGGGAAATATAGATAGACACTGGAATGGCCATTTGGACACTTGGCCCC 3092
QY 3436 ACTGAGACAACTATTCCTGAGAGAGTGGCTGGG -CCCGAGCTCTCTCCCTGTGAC 3494
DB 3093 ACTGAGACAACTATTCCTGAGAGAGTGGCTGGG -CCCGAGCTCTCTCCCTGTGAC 3152
QY 3495 ACACCTGACCCCACTGCTGAGAACTGTGGGGTGAAGAGAGCAAGAGAGGAAATG 3554
DB 3153 ACACCTGACCCCACTGCTGAGAACTGTGGGGTGAAGAGAGCAAGAGAGGAAATG 3212
QY 3555 TTTCCTGTGCTGCTCTCTCTGACTTGTCTGACTTGTGGGCTTCTTCTCTCTCATCACT 3614
DB 3213 TTTCCTGTGCTGCTCTCTCTGACTTGTCTGACTTGTGGGCTTCTTCTCTCTCATCACT 3272
QY 3615 GAAACACTGAGCTGGGGGTAGCCCGCCGAGCCCTCAGTACACCCCATCTCCACTG 3674
DB 3273 GAAACACTGAGCTGGGGGTAGCCCGCCGAGCCCTCAGTACACCCCATCTCCACTG 3332
QY 3675 CAGTCTGTAGCTAGAACTTCTCTAAGCTTATAGCTTCTGTGAGTAAATATTGGGATT 3734
DB 3333 CAGTCTGTAGCTAGAACTTCTCTAAGCTTATAGCTTCTGTGAGTAAATATTGGGATT 3392
QY 3735 GGGGGGAAAGAGGAGCAACGCGCCCATAGCTTGGGGTGTGACATCTCTAATGTAGCTGC 3794
DB 3393 GGGGGGAAAGAGGAGCAACGCGCCCATAGCTTGGGGTGTGACATCTCTAATGTAGCTGC 3452
QY 3795 CACATTTATTTTCTAATACACTTGGGGTTTGTACATTTTGGGGGAGAGACAGAT 3854
DB 3453 CACATTTATTTTCTAATACACTTGGGGTTTGTACATTTTGGGGGAGAGACAGAT 3512
QY 3855 TTTTACACTAATATATGAGCACTTGTAGGCAATTTTATCCCTCAGTACAGGAGTA 3914
DB 3513 TTTTACACTAATATATGAGCACTTGTAGGCAATTTTATCCCTCAGTACAGGAGTA 3572
QY 3915 ATATATAAGGTGAGTTTCCACAAATAAAAAAAAAA 3953
DB 3573 ATATATAAGGTGAGTTTCCACAAATAAAAAAAAAA 3611

RESULT 8
ARI03004 ARI03004 3637 bp DNA linear PART 14-FEB-2001
DEFINITION Sequence 3 from patent US 6087144.

[illegible]

QY	1036	ATGACCTTTAGGAAGAGTACAGAGAGCTGGGGGCTCTGAGCCAGGCTATGACTATGTGGAGATGGA	10939
Db	797	ATGACCTTTAGGAAGAGTACAGAGAGCTGGGGGCTCTGAGCCAGGCTATGACTATGTGGAGATGGA	856
QY	1096	GCACACACAGCTTCTCCAGTGGCATGTGGAGAGATGGAGTTTGAATTGACCGCGAGAGG	11555
Db	857	GCACACACAGCTTCTCCAGTGGCATGTGGAGAGATGGAGTTTGAATTGACCGCGAGAGG	916
QY	1156	CCTTCAGGCTATGCAAGGTTCACATGTAAACAATGACACAGCTGAGAGCCGCTGTGCCTG	12151
Db	917	CCTTCAGGCTATGCAAGGTTCACATGTAAACAATGACACAGCTGAGAGCCGCTGTGCCTG	976
QY	1216	GGGGGGTGGAAATGTGCTCTCCGGCGTGCCCTGCCATGSGCTGGAGGGGGAGCCCATGC	12757
Db	977	GGGGGGTGGAAATGTGCTCTCCGGCGTGCCCTGCCATGSGCTGGAGGGGGAGCCCATGC	10386
QY	1276	GCACACACCTAGGGGGGCAACCTGGGGGGACCCACAGAGCCGGGGGTGCTATAGTCCCCCTTG	13353
Db	1037	GCACACACCTAGGGGGGCAACCTGGGGGGACCCACAGAGCCGGGGGTGCTATAGTCCCCCTTG	10986
QY	1336	GGGGCGGTGTGGCTTCCTTTCTGCAAGTCCGCTTCCTTTGGGGGGCCCTGGTTACTCT	13959
Db	1097	GGGGCGGTGTGGCTTCCTTTCTGCAAGTCCGCTTCCTTTGGGGGGCCCTGGTTACTCT	11566
QY	1396	TGAGGAAATCTCCTTCACTCTCTATGTGTGTAACAATTCCTCTCCGACATGGAGGACA	14555
Db	1157	TGAGGAAATCTCCTTCACTCTCTATGTGTGTAACAATTCCTCTCCGACATGGAGGACA	12166
QY	1456	CCCTCCGGCGAGCCCGCTGGTGGCGGCGCTGGCCCACTCCACACAATTCAAGACTTGG	15151
Db	1217	CCCTCCGGCGAGCCCGCTGGTGGCGGCGCTGGCCCACTCCACACAATTCAAGACTTGG	12766
QY	1516	ACCTGAGACCCAGAGAGCCAGAGCCCTGGCCACAAGGCCGAGGGAGCCGACCGCATTC	15757
Db	1277	ACCTGAGAGCCAGAGAGCCAGAGCCCTGGCCACAAGGCCGAGGGAGCCGACCGCATTC	13366
QY	1576	TCATGCGCTGCCGTGGTGCCATCATCTGCTCTGTGCTCATATTTGCCCTCATGCTCT	16353
Db	1337	TCATGCGCTGCCGTGGTGCCATCATCTGCTCTGTGCTCATATTTGCCCTCATGCTCT	13966
QY	1636	GGCGGCTGCATGCGCGCAGAGGTCTCTACGCAAGGCTCAAGAGAGGTGTGGAAGAGAGC	16953
Db	1397	GGCGGCTGCATGCGCGCAGAGGTCTCTACGCAAGGCTCAAGAGAGGTGTGGAAGAGAGC	14566
QY	1696	TACAGGTTCACTCTCTGTCCGCTGGGGACACTTCTCATCAACAACCGCCAGGTCTCTA	17555
Db	1457	TACAGGTTCACTCTCTGTCCGCTGGGGACACTTCTCATCAACAACCGCCAGGTCTCTA	15166
QY	1756	GAGAGCACCCCGGTACAGAGAGCCCGGCTGTGGGAATCCGCGCCACTCGCTCCCT	18151
Db	1517	GAGAGCACCCCGGTACAGAGAGCCCGGCTGTGGGAATCCGCGCCACTCGCTCCCT	15766
QY	1816	GTGTCCCAAGGSGTCTGCGTGTGTGTGTCTCTCCATACAGACTACCGGCTCTTGTGGCA	18751
Db	1577	GTGTCCCAAGGSGTCTGCGTGTGTGTGTCTCTCCATACAGACTACCGGCTCTTGTGGCA	16366
QY	1876	CTTACGCCCTGCCCCCTCGAGAGCCCGGGCCCCCACAACCGGCTGGGGCAAAACCAACA	19351
Db	1637	CTTACGCCCTGCCCCCTCGAGAGCCCGGGCCCCCACAACCGGCTGGGGCAAAACCAACA	16966
QY	1936	ACACCCAGGCTTACAGTGGGAGCTATATGAGAGCTGAGAGCCAGCGCCCCCGGCTTGTGC	19951
Db	1697	ACACCCAGGCTTACAGTGGGAGCTATATGAGAGCTGAGAGCCAGCGCCCCCGGCTTGTGC	17566
QY	1996	CCCCACTCCCCAGAACAGGCTCCCCCATTTATGCGAGGGCTGACATTGTTACCTCGAGG	20551
Db	1757	CCCCACTCCCCAGAACAGGCTCCCCCATTTATGCGAGGGCTGACATTGTTACCTCGAGG	18166
QY	2056	GCCTACCGGGGGGACAACCTATGCTGTGTCGACATCGCCCCAGAGGGGCAATGGGGGATG	21151
Db	1817	GCCTACCGGGGGGACAACCTATGCTGTGTCGACATCGCCCCAGAGGGGCAATCGGGGATG	18766
QY	2116	GGCCCCCAGAGTGAATTCCTCCATCTCGACTCGGCTTCAAGAGAGAGTTGGCGAGG	21751

Db	1877	GGCCCCCAGAGGTGATTTCCCTCGATCTCGATCCGCTTCAAGGAGAACTTGGCGAGG	1936
QY	2176	GCACGTTTGGGAGGTGCACCTGTGAGAGGTGCACAGCCCTCAAGATCTGGCTACTTGG	2235
Db	1937	GCACGTTTGGGAGGTGCACCTGTGAGAGGTGCACAGCCCTCAAGATCTGGCTACTTGG	1996
QY	2236	ATTTCGCCCTTAATGTGCTAAGGGACACCCCTTGCCTGTACTGTCAAGATCTTAACGC	2239
Db	1997	ATTTCGCCCTTAATGTGCTAAGGGACACCCCTTGCCTGTACTGTCAAGATCTTAACGC	2056
QY	2236	CAGATGCCACCAAGATGCCAGCTTCTCTGTCTCCAGAAATGATTTCTGAAAGAG	2355
Db	2057	CAGATGCCACCAAGAAAG-----CCAGGAATGATTTCTGAAAGAG	2098
QY	2356	TGAAGATCATGTGAGAGCTCAAGAGCCCAACATCATTTGGTGGCTGGGCGTGTGTGAC	2415
Db	2099	TGAAGATCATGTGAGAGCTCAAGAGCCCAACATCATTTGGTGGCTGGGCGTGTGTGAC	2158
QY	2416	AGGACGACCCCTCTGTGCATGATTACTGACTACATGGAGAAGCGGACCTCAACAGTTCC	2479
Db	2159	AGGACGACCCCTCTGTGCATGATTACTGACTACATGGAGAAGCGGACCTCAACAGTTCC	2218
QY	2476	TCAATGGCCACACAGCTGGAGAGAACAGCGAGGGGGCCCTGGGACGGGACGCTG	2535
Db	2219	TCAATGGCCACACAGCTGGAGAGAACAGCGAGGGGGCCCTGGGACGGGACGCTG	2278
QY	2536	CGCAGGGGCCACCATCAGCTACCCCATGCTGTGTGANTGTGGACCCAGATCCGCTCG	2599
Db	2279	CGCAGGGGCCACCATCAGCTACCCCATGCTGTGTGANTGTGGACCCAGATCCGCTCG	2338
QY	2596	GCATGGCCCTATCTGGCCACACTAATTTGTATCTGGGAACTGGCCACGCGGAATGCC	2655
Db	2339	GCATGGCCCTATCTGGCCACACTAATTTGTATCTGGGAACTGGCCACGCGGAATGCC	2398
QY	2656	TAGTTGGGGAAAATTTCCACCATCAAAATGCGAGACTTTGGCATGAGCGGAACTCTATG	2715
Db	2399	TAGTTGGGGAAAATTTCCACCATCAAAATGCGAGACTTTGGCATGAGCGGAACTCTATG	2458
QY	2716	CTGGGGGACTATTACCGTGTGCAGAGGCGGGGCGAGTGTGCCATCCGCTGGATGCCCTGG	2775
Db	2459	CTGGGGGACTATTACCGTGTGCAGAGGCGGGGCGAGTGTGCCATCCGCTGGATGCCCTGG	2518
QY	2776	AGTCAATCTCATATGGGGAAATTCACAGCTGCGAGTACACTGTGGGCGTTTGGTGTGACC	2835
Db	2519	AGTCAATCTCATATGGGGAAATTCACAGCTGCGAGTACACTGTGGGCGTTTGGTGTGACC	2578
QY	2836	TGTGGAGGTGCTGATGCTCTGTAGGGGCCACAGCCCTTGGGAGCTCAACGACGACAG	2895
Db	2579	TGTGGAGGTGCTGATGCTCTGTAGGGGCCACAGCCCTTGGGAGCTCAACGACGACAG	2638
QY	2896	TCAATCGAAGACGGGGGGGAATTTCTCCGGGACACAGGGCGGAGGTATATCTGTCCGGC	2955
Db	2639	TCAATCGAAGACGGGGGGGAATTTCTCCGGGACACAGGGCGGAGGTATATCTGTCCGGC	2698
QY	2956	CGCCTGCTCCCGCAGGGGCTATATGACCTATGCTTCGTGGTGTGAGACGGGAGTGTG	3015
Db	2699	CGCCTGCTCCCGCAGGGGCTATATGACCTATGCTTCGTGGTGTGAGACGGGAGTGTG	2758
QY	3016	AGCAGGACACCCCTTTCCCACTGCTCATCGGTTCCCTGGCAGAGGATGCACCTCAACAGG	3075
Db	2759	AGCAGGACACCCCTTTCCCACTGCTCATCGGTTCCCTGGCAGAGGATGCACCTCAACAGG	2818
QY	3076	TGTAAATCAACAATCCAGAGCCCGCTTCAGAGGAGTGATCAGGGGAAAGCAAGTAGCA	3135
Db	2819	TGTAAATCAACAATCCAGAGCCCGCTTCAGAGGAGTGATCAGGGGAAAGCAAGTAGCA	2878
QY	3136	CTAAACAGAGAGACAAATGGGACCTCTGACCCTTCCCTCCGACAGCCCATCACTCT	3195
Db	2879	CTAAACAGAGAGACAAATGGGACCTCTGACCCTTCCCTCCGACAGCCCATCACTCT	2938
QY	3196	AATAGAGCAGTAGACTCGAGGTGGGCTGGGGCCACCAAGGAGCTATATGCCCTTCTC	3255

Db	2939	AATAGAGGAGTGAACACTGC-----	2958
QY	3256	CCCTTCCTGGACACACTCTCATGTGCCCTTCTGTCTTCTTCTCTAGAACCCCTGTGC	3315
Db	2959	-----AGAAAGCCCTCTGTGC	2972
QY	3316	CCACCCAGACTGGTCTGTGGATGGGATCCTCCACCCCTCCTCTAGGCATCCCTTGGGG	3375
Db	2973	CCCAACCACTGTGTCTGTGGATGGGATCCTTCCACCCCTCCTCTAGGCATCCCTTGGGG	3032
QY	3376	AAGGTTGGGGAAATATATAGATAGACACTGACATATGCCCCATTTGGAGCACCCTGGGGCCC	3435
Db	3033	AAGGTTGGGGAAATATATAGATATACACTGACATATGCCCCATTTGGAGCACCCTGGGGCCC	3092
QY	3436	ACTGCACACACTGATTTCCGTGGAGAGTGTGCG-CCCCAGCTTCTCTCTCCGTGCAC	3494
Db	3093	ACTGCACACACTGATTTCCGTGGAGAGTGTGCGCCCCCAGCTTCTCTCTCCGTGCAC	3152
QY	3495	ACACGTGGACCCACATGGCTGAGAACTGGGGGTGAGAGAGACAAAGAGAGGAGAAATG	3554
Db	3153	ACACGTGGACCCACATGGCTGAGAACTGGGGGTGAGAGAGACAAAGAGAGGAGAAATG	3212
QY	3555	TTTCCTTGTGCTGCTCCTGTACTGTGCTCAGCTTGGGCTCTCTCTCCTCATCAGCT	3614
Db	3213	TTTCCTTGTGCTGCTCCTGTACTGTGCTCAGCTTGGGCTCTCTCTCCTCATCAGCT	3272
QY	3615	GAACACGTGGACCTGGGGGTAGCCCCGCCGCCAGCCCTGAGTACCCCACTTCCAGCTTG	3674
Db	3273	GAACACGTGGACCTGGGGGTAGCCCCGCCGCCAGCCCTGAGTACCCCACTTCCAGCTTG	3332
QY	3675	CAGTCTGTAGCTAAGCTTCTCTCTAAGCCTAATAGCTTTCTGTGAGTAAATTTGGGAT	3734
Db	3333	CAGTCTGTAGCTAAGCTTCTCTCTAAGCCTAATAGCTTTCTGTGAGTAAATTTGGGAT	3392
QY	3735	GGGGGGAAGAGGAGCAACGGCCCATATGCTTGGGGGTGAGACATCTAGTGTAGCTGC	3794
Db	3393	GGGGGGAAGAGGAGCAACGGCCCATATGCTTGGGGGTGAGACATCTAGTGTAGCTGC	3452
QY	3795	CACATTTGATTTTCTATATATCACTTGGGGTTGTACATTTTGGGGGAGAGACACAGAT	3854
Db	3453	CACATTTGATTTTCTATATATCACTTGGGGTTGTACATTTTGGGGGAGAGACACAGAT	3512
QY	3855	TTTTACATTAATATATGAGACCTGAGCAATTTAATCCCTGCACTAGGAGGTA	3914
Db	3513	TTTTACATTAATATATGAGACCTGAGCAATTTAATCCCTGCACTAGGAGGTA	3572
QY	3915	ATAATTAAGGTGAGTTTCCACAATAAAAAAAAAAAAAA	3953
Db	3573	ATAATTAAGGTGAGTTTCCACAATAAAAAAAAAAAAAA	3611

RESULT	9			
AR105288				
LOCUS	AR105288	3637 bp	DNA	linear
DEFINITION	Sequence 3 from patent US 6096527.			
ACCESSION	AR105288			
VERSION	AR105288.1	GI:12818885		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 3637)			
TITLE	Godowski, P.J., Mark, M.R. and Scadden, D. ".			
JOURNAL	Nucleic acids encoding protein tyrosine kinases			
FEATURES	Patent: US 6096527-A 3 01-AUG-2000;			
SOURCE	Location/Qualifiers			
	1..3637			
	/organism="unknown"			
BASE COUNT	721 a	1094 c	1079 g	743 t
ORIGIN				

Query Match 87.1%; Score 3451; DB 6; Length 3637;

Best Local Similarity 97.0%; Pred. No. 0;
Matches 3589; Conservative 0; Mismatches 5;
Indels 105; Gaps 3;

QY	256	GTGGAGACTGMAAGGAATGCCAAGAATGCTGCCCCACCCCTTAAGGCCCGAGGATCAG	315
Db	17	GTGGAGACTGMAAGGAATGCCAAGAATGCTGCCCCACCCCTTAAGGCCCGAGGATCAG	76
QY	316	GAGCTATGGACACAGAGGCCCTGTATCTTTAAGTCTGCTCTCTCTGTGGTGGCAGTGGAG	375
Db	77	GAGCTATGGACACAGAGGCCCTGTATCTTTAAGTCTGCTCTCTCTGTGGTGGCAGTGGAG	136
QY	376	ATGCTGACATGAAGGGACATTTTGTATCCCTGCCAATGGCCGCTATAGCCCTGGGCATATCAGC	435
Db	137	ATGCTGACATGAAGGGACATTTTGTATCCCTGCCAATGGCCGCTATAGCCCTGGGCATATCAGC	136
QY	436	ACCGGACCATCCCAAGACACTAGCTCTCTCTCTCCAGCTCCTGTGATCAATTCACATGCCG	495
Db	197	ACCGGACCATCCCAAGACACTAGCTCTCTCTCTCCAGCTCCTGTGATCAATTCACATGCCG	256
QY	496	CCCGCACACGACAGTGTGGAGACACTGACGGGGAATGGGGCCCTGGTGGCCCGCAGGGTCGG	555
Db	257	CCCGCACACGACAGTGTGGAGACACTGACGGGGAATGGGGCCCTGGTGGCCCGCAGGGTCGG	316
QY	556	TGTTTCCCAAGAGGAGGAGTACTTTCAGGTGATCTTACAACGACTCCACCTGGTGGCTC	615
Db	317	TGTTTCCCAAGAGGAGGAGTACTTTCAGGTGATCTTACAACGACTCCACCTGGTGGCTC	376
QY	616	TGGTGGGACCCAGGAGGACGCACTCCGGGGCCCTGGGCAAGAGATTCTCCGAGCTACC	675
Db	377	TGGTGGGACCCAGGAGGACGCACTCCGGGGCCCTGGGCAAGAGATTCTCCGAGCTACC	436
QY	676	GGCTGGTACTCCCGGAGTGGTCGCGCCTGGATGGGTGGGAAGACGCGTGGGGTACAG	735
Db	437	GGCTGGTACTCCCGGAGTGGTCGCGCCTGGATGGGTGGGAAGACGCGTGGGGTACAG	496
QY	736	AGGTGATCTCAGGCAATGAGAACCCCTGAAGGAGTGGTCTTGAAGACCTTGGGCCCCCA	795
Db	497	AGGTGATCTCAGGCAATGAGAACCCCTGAAGGAGTGGTCTTGAAGACCTTGGGCCCCCA	556
QY	796	TGGTGGCCGAGCTGGTTCGCTTACACCCCGGGGCTGACCGGGTCAATGATGTCTGTCTGC	855
Db	557	TGGTGGCCGAGCTGGTTCGCTTACACCCCGGGGCTGACCGGGTCAATGATGTCTGTCTGC	616
QY	856	GGGTAGAGCTATAGGCTGCTCTGAGAGGATGAGACTCTGTCTTACACCGCCCTGTGG	915
Db	617	GGGTAGAGCTATAGGCTGCTCTGAGAGGATGAGACTCTGTCTTACACCGCCCTGTGG	676
QY	916	GGCAACAAATGATTTATCTGAGCCGTGTACCTCAACGACTCCACCTATGACGACATATA	975
Db	677	GGCAACAAATGATTTATCTGAGCCGTGTACCTCAACGACTCCACCTATGACGACATATA	736
QY	976	CCGTGGGGGAGCTGAGATAGGGGGGTGTGGGGCAGCGTGGAGATGGTGTGGGGCTGG	1035
Db	737	CCGTGGGGGAGCTGAGATAGGGGGGTGTGGGGCAGCGTGGAGATGGTGTGGGGCTGG	796
QY	1036	ATGACTTTAGGAAGAGTACAGAGGTGCGGGTCTGGCCAGGCTATGACTATGTGGAGTGA	1095
Db	797	ATGACTTTAGGAAGAGTACAGAGGTGCGGGTCTGGCCAGGCTATGACTATGTGGAGTGA	856
QY	1096	GCAACACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAATTGACCGGCTGAGGG	1155
Db	857	GCAACACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAATTGACCGGCTGAGGG	916
QY	1156	CTTTCACAGCTATGACAGTGCACGTGTAAACAATGCAACGCGTGGGAGAGCCGCTGACCTG	1215
Db	917	CTTTCACAGCTATGACAGTGCACGTGTAAACAATGCAACGCGTGGGAGAGCCGCTGACCTG	976
QY	1216	GGGGGTGGAATGTCTGCTCCGGCTGGGCCCTCCATGGCTGTGGAGAGGGAGAGCCATATG	1275
Db	977	GGGGGTGGAATGTCTGCTCCGGGTGGGCCCTCCATGGCTGTGGAGAGGGAGAGCCATATG	1036
QY	1276	GGCAACACTTAGGGGGCAACCTGGGGGACCCCAAGACCCGGGCTGTCTCAGTCCCTTGG	1335

Db	1037	GCACACACTTGAAGGGGGACCACTGGGGGAGCCCAAGACGCCGGGCTGTCTCAATGAGCCCTTGG	1099
QY	1336	GGGGCCGTGTGGCTCGCTTCTTGCAATGACCGCTCTCTTGGCGGGGCCCTGGTTACTCT	1395
Db	1097	GGGGCCGATGTGGCTCGCTTCTTGCAATGAGCCGCTTCCTTGGGGGGCCCTGGTTACTCT	1150
QY	1396	TCAGGGAATCTCCTCATCTCTCATGTGTGGTGAACAATTCTCTCCGGCACTGGGAGGCA	1455
Db	1157	TCAGGGAATCTCCTCATCTCTCATGTGTGGTGAACAATTCTCTCCGGCACTGGGAGGCA	1218
QY	1456	CCCTCCCGGACCCCGCTGGTGGCGGCGCTGGCCACCTCCACCACTTCAGAGATTGG	1515
Db	1217	CCCTCCCGGACCCCGCTGGTGGCGGCGCTGGCCACCTCCACCACTTCAGAGATTGG	1278
QY	1516	ACCTGAGCCCAAGAGGCCAGCGCCGTGGGCCAAGGCCGAGGGGAGCCCGACCGCATCC	1579
Db	1277	ACCTGAGCCCAAGAGGCCAGCGCCGTGGGCCAAGGCCGAGGGGAGCCCGACCGCATCC	1338
QY	1576	TCATGGGCTGGCTGGTGGCCATCATCTGCTCCTGCTGCTCAATTCAGCCCTCAATGCTCT	1635
Db	1337	TCATGGGCTGGCTGGTGGCCATCATCTGCTCCTGCTGCTCAATTCAGCCCTCAATGCTCT	1386
QY	1636	GGCGGCTGCTAGTGGCGAGCGCTCTCTCAGCAAGGCTGAAGAGGTTGTGAAGAGAGAC	1693
Db	1397	GGCGGCTGCTAGTGGCGAGCGCTCTCTCAGCAAGGCTGAAGAGGTTGTGAAGAGAGAC	1456
QY	1696	TCACGGTTCACACTCTCTGTCTCTGTGGGACACTTCTCATCAACAACCGCCCAAGTCTCTA	1755
Db	1457	TCACGGTTCACACTCTCTGTCTCTGTGGGACACTTCTCATCAACAACCGCCCAAGTCTCTA	1516
QY	1756	GAGAGCCACCCCGCTTACAGAGAGCCCGGCGCTGTGGGAATCGCCGCCCTCGGTCCT	1815
Db	1517	GAGAGCCACCCCGCTTACAGAGAGCCCGGCGCTGTGGGAATCGCCGCCCTCGGTCCT	1576
QY	1816	GTGTCCCAATGCTCTGTGCTGTGCTCTCAATCCAGCTTACCGGCTCTTGTGGCCA	1875
Db	1577	GTGTCCCAATGCTCTGTGCTGTGCTCTCAATCCAGCTTACCGGCTCTTGTGGCCA	1636
QY	1876	CTTAAAGCCCGTCCCGCTCGAGGGCCGGGGCCCGCCACACCGGCGTGGGCAAAACCCACA	1935
Db	1637	CTTAAAGCCCGTCCCGCTCGAGGGCCGGGGCCCGCCACACCGGCGTGGGCAAAACCCACA	1586
QY	1936	ACACCCAGGCTTACAGTGGGAGCTATATGAGAGCTTGAAGCCAGCGCCCGCTTCTGTC	1995
Db	1697	ACACCCAGGCTTACAGTGGGAGCTATATGAGAGCTTGAAGCCAGCGCCCGCTTCTGTC	1756
QY	1996	CCCAACCTCCCAAGAGGTCGCCCATTTAATGCGAGGCTGACATTTGTACCTGCAAG	2055
Db	1757	CCCAACCTCCCAAGAGGTCGCCCATTTAATGCGAGGCTGACATTTGTACCTGCAAG	1816
QY	2056	GGCTACCGGGGGCAACACTATGTGTGCTGCACTGCGCCCAAGGCGCACTCGGGATG	2115
Db	1817	GGCTACCGGGGGGGCAACACTATGTGTGCTGCACTGCGCCCAAGGCGCACTCGGGATG	1876
QY	2116	GGCCCCCAAGTGGATTTCCCTCGATCTTCGACTCGCTTCAAGGAGAGCTTGGCAGG	2175
Db	1877	GGCCCCCAAGTGGATTTCCCTCGATCTTCGACTCGCTTCAAGGAGAGCTTGGCAGG	1936
QY	2176	GCCAGTTTGGGAGTGCACCTGTGTGAGTGTGACAGCCCTCAAGTATGGTCAAGTCTTG	2235
Db	1937	GCCAGTTTGGGAGTGTACACTGTGTGAGTGTGACAGCCCTCAAGTATGGTCAAGTCTTG	1996
QY	2236	ATTTCCCTTAAATGTGCTGAAGGACACCTTGTCTGTGTAGCTGTCAAGATCTTACAGC	2295
Db	2296	ATTTCCCTTAAATGTGCTGAAGGAGACACCTTGTCTGTGTAGCTGTCAAGATCTTACAGC	2056
QY	2057	CAGATGCCACCAAGAAATGCGAGTTCCTCTTCCAGAAATGATTTCTGAAAGAGG	2355
Db	2356	TGAAGATCATGTGAGGCTCAAGAGACCCCAACATCATTCGGCTGTGGGCTGTGTGTC	2415
QY	2415	TGAAGATCATGTGAGGCTCAAGAGACCCCAACATCATTCGGCTGTGGGCTGTGTGTC	2158

QY 2416 AGAGAGACCCCTCTGATGATTTACTACTATGAGAGAGGCGACCTCAACAGTTC 2475
 DB 2159 AGAGAGACCCCTCTGATGATTTACTACTATGAGAGAGGCGACCTCAACAGTTC 2218
 QY 2476 TCAGTCCCGACAGAGTGGAGAGCAAGGACCGAGGGGGCCCTGGGAGGCGAGCTG 2535
 DB 2219 TCAGTCCCGACAGAGTGGAGAGCAAGGACCGAGGGGGCCCTGGGAGGCGAGCTG 2278
 QY 2536 CGCAGAGGCGCCACATGACTACCAATGCTGCTGATGGAGCCGAGATCCGCTCG 2595
 DB 2279 CGCAGAGGCGCCACATGACTACCAATGCTGCTGATGGAGCCGAGATCCGCTCG 2338
 QY 2596 GCATGCGCTATCTGGCCACACTCACTTTGATATCGGAGCTGGCCAGCGGAGTCC 2655
 DB 2339 GCATGCGCTATCTGGCCACACTCACTTTGATATCGGAGCTGGCCAGCGGAGTCC 2398
 QY 2656 TAGTGGGGGAAATTTCAACATCAAAATCGCAGACTTTGGCATGAGCCGAACTCTATG 2715
 DB 2399 TAGTGGGGGAAATTTCAACATCAAAATCGCAGACTTTGGCATGAGCCGAACTCTATG 2458
 QY 2716 CTGGGAGCTATTTACCGTGTGAGGCGCGGAGTGTGCTCCATCCGCTGATGGCTGGG 2775
 DB 2459 CTGGGAGCTATTTACCGTGTGAGGCGCGGAGTGTGCTCCATCCGCTGATGGCTGGG 2518
 QY 2776 AGTGCATCTCATGAGGGAAGTTCACAGACTGCGAGTGCAGTGTGGCCCTTTGGTGTGACC 2835
 DB 2519 AGTGCATCTCATGAGGGAAGTTCACAGACTGCGAGTGCAGTGTGGCCCTTTGGTGTGACC 2578
 QY 2836 TGTGGGAGTGTCTGATGCTCTGTAGGGCCGACCCCTTTGGGAGCTCACGACAGAGG 2895
 DB 2579 TGTGGGAGTGTCTGATGCTCTGTAGGGCCGACCCCTTTGGGAGCTCACGACAGAGG 2638
 QY 2896 TCATCGAAGACGGGGGAGTTCTCCGGAGCAGAGGCGCGGAGTGTACCTGTCCCGGC 2955
 DB 2639 TCATCGAAGACGGGGGAGTTCTCCGGAGCAGAGGCGCGGAGTGTACCTGTCCCGGC 2698
 QY 2956 CGCCTGCTGCGCCGAGGCGCTATATGAGCTGATGCTGCTGTGAGCGGGAGTCTG 3015
 DB 2699 CGCCTGCTGCGCCGAGGCGCTATATGAGCTGATGCTGCTGTGAGCGGGAGTCTG 2758
 QY 3016 AGCAGCGACACCCCTTTTCCAGCTGCACTCGTTCCTGGCAGAGAGTCACTCAACGCG 3075
 DB 2759 AGCAGCGACACCCCTTTTCCAGCTGCACTCGTTCCTGGCAGAGAGTCACTCAACGCG 2818
 QY 3076 TGTGAATCACACATCAAGCTGCCCCCTCCAGGAGGATCCAGGGGAAAGCCAGTACA 3135
 DB 2819 TGTGAATCACACATCAAGCTGCCCCCTCCAGGAGGATCCAGGGGAAAGCCAGTACA 2878
 QY 3136 CTAAAGCAAGAGACATGAGCACTGCTCCCTCCCTCCGACAGCCCATCACTCT 3195
 DB 2879 CTAAAGCAAGAGACATGAGCACTGCTCCCTCCCTCCGACAGCCCATCACTCT 2938
 QY 3196 AATGAGAGCAGTGAAGTGCAGAGTGGGCTGGGCCACACAGGAGTGAATGCCCTTCTC 3255
 DB 2939 AATGAGAGCAGTGAAGTGCAGAGTGGGCTGGGCCACACAGGAGTGAATGCCCTTCTC 2958
 QY 3256 CCTTCTCGAGACACTCTATGTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 3315
 DB 2959 CCTTCTCGAGACACTCTATGTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 2972
 QY 3316 CCCACCCAGCTGCTCTGTGATGAGATCCCTTCCACCTCTCTCTCTCTCTCTCTCTCTG 3375
 DB 2973 CCCACCCAGCTGCTCTGTGATGAGATCCCTTCCACCTCTCTCTCTCTCTCTCTCTCTG 3032
 QY 3376 AAGGCTGGGGAATATAGATAGACATGAGCATGGCCCATTTGAGCAGCTGGGCCCC 3435
 DB 3033 AAGGCTGGGGAATATAGATAGACATGAGCATGGCCCATTTGAGCAGCTGGGCCCC 3092
 QY 3436 ACTGAGACAACACTGATCTCTGAGAGGCTGGCTGG-CCCGAGCTCTCTCTCTCTCTCTCT 3494
 DB 3093 ACTGAGACAACACTGATCTCTGAGAGGCTGGCTGG-CCCGAGCTCTCTCTCTCTCTCTCT 3152

QY 3495 ACACGTGACCCCACTGCTGAGAAATCTGGGGTGGAGAGCAGCAAGAGAGGAAATG 3554
 DB 3153 ACACGTGACCCCACTGCTGAGAAATCTGGGGTGGAGAGCAGCAAGAGAGGAAATG 3212
 QY 3555 TTTCCTTGTCCCTGCTCTCTGATCTTGTCTGAGCTTTGGGCTTCTCTCTCTCTCTCT 3614
 DB 3213 TTTCCTTGTCCCTGCTCTCTGATCTTGTCTGAGCTTTGGGCTTCTCTCTCTCTCTCT 3272
 QY 3615 GAACACATGAGACCTGGGGGTAGCCCGCCGACCCCTAGTCACCCCACTTCCACTTG 3674
 DB 3273 GAACACATGAGACCTGGGGGTAGCCCGCCGACCCCTAGTCACCCCACTTCCACTTG 3332
 QY 3675 CAGCTTGTAGCTGAACTTCTCTAGCCCTTCTCTAGCTTTCTGTGAGTAAATTTGGGAT 3734
 DB 3333 CAGCTTGTAGCTGAACTTCTCTAGCCCTTCTCTAGCTTTCTGTGAGTAAATTTGGGAT 3392
 QY 3735 GGGGGGAAAGAGGAGCAGAGGCGCCCAATAGCCTTGGGGTTGACATCTCTAGTACTGC 3794
 DB 3393 GGGGGGAAAGAGGAGCAGAGGCGCCCAATAGCCTTGGGGTTGACATCTCTAGTACTGC 3452
 QY 3795 CACATGATTTTCTCTATATACACTTGGGGTTGTGATCTTTTGGGGGAGAGACACAT 3854
 DB 3453 CACATGATTTTCTCTATATACACTTGGGGTTGTGATCTTTTGGGGGAGAGACACAT 3512
 QY 3855 TTTTACACTAATATATGAGACCTAGCTGAGCAATTTTATCCCTGACACTAGCAGGTA 3914
 DB 3513 TTTTACACTAATATATGAGACCTAGCTGAGCAATTTTATCCCTGACACTAGCAGGTA 3572
 QY 3915 ATAAATTAAGTTGAGTTTCCACAAAAAATTTTAAAAA 3953
 DB 3573 ATAAATTAAGTTGAGTTTCCACAAAAAATTTTAAAAA 3611

RESULT 10
 180845
 LOCUS 180845 3637 bp DNA linear PAT 10-JUN-1998
 DEFINITION Sequence 3 from patent US 5709858.
 ACCESSION 180845
 VERSION 180845.1 GI:3209135
 KEYWORDS
 SOURCE
 ORGANISM
 UNKNOWN.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 3637)
 AUTHORS Godowski,P.J., Mark,M.R. and Scadden,D.T.
 TITLE Antibodies specific for Rse receptor protein tyrosine kinase
 JOURNAL Patent: US 5709858-A 3 20-JAN-1998;
 FEATURES
 source 1..3637
 BASE COUNT 721 a 1094 c 1079 g 743 t
 ORIGIN

Query Match 87.1%; Score 3451; DB 6; Length 3637;
 Best Local Similarity 97.0%; Pred. No. 0;
 Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;
 QY 256 GTTGACTTGAAGGAATCCAGAGATGCTGCCACCCCTTAGGCCGAGGATCAG 315
 DB 17 GTTGACTTGAAGGAATCCAGAGATGCTGCCACCCCTTAGGCCGAGGATCAG 76
 QY 316 GAGCTATGGAGCAGAGAGCCCTGTCATCTTACTGCTGCTCTTGGTGGCAAGTGGAG 375
 DB 77 GAGCTATGGAGCAGAGAGCCCTGTCATCTTACTGCTGCTCTTGGTGGCAAGTGGAG 136
 QY 376 ATGCTGACATGAAGGAGACATTTTATGCTGCAAGTCCCGATATGCCCTGGAGTGCAG 435
 DB 137 ATGCTGACATGAAGGAGACATTTTATGCTGCAAGTCCCGATATGCCCTGGAGTGCAG 196
 QY 436 ACCGAGACATCCAGAGAGTGCATCTCTGCTTCCAGCTCTGTGATTCAGATTCAGTCCG 495
 DB 197 ACCGAGACATCCAGAGAGTGCATCTCTGCTTCCAGCTCTGTGATTCAGATTCAGTCCG 256

QY	496	CCCGCCACAGCAGCTTGGAGAGCAGTGCACGGGATGGGGCTGTGTCCCGCAGAGGTGG	555
Db	257	CCCCGCACAGCAGGTGGAGAGCAGTACACGGGGATGGGGCTGTGTCCCGCAGAGGTGG	316
QY	556	TGTTTCCCAAGAGAGAGAGACTTGCAGAGTGGATCTCAACAGACTCAACTGGTGGCTC	615
Db	317	TGTTTCCCAAGAGAGAGAGACTTGCAGAGTGGATCTCAACAGACTCAACTGGTGGCTC	376
QY	616	TGGTGGACACCCAGGGAGCGCATGCCGGGGGCTGGGCAAGAGATTCTCCCGAGCTAC	675
Db	377	TGGTGGAGACCCAGGGAGCGCATGCCGGGGGCTGGGCAAGAGATTCTCCCGAGCTAC	436
QY	676	GGCTCGTTACTCCCGGGATGGTGGCGGTGAGTGGGCTGGGAAGAGACCGTGGGGTCAAG	735
Db	437	GGCTCGTTACTCCCGGGATGGTGGCGGTGAGTGGGCTGGGAAGAGACCGTGGGGTCAAG	496
QY	736	AGTGATATCTCAGGCATATGAGAGACCTTAGAGGAGTGGTGTGAAGAGACTTGGGGCCCCA	795
Db	497	AGTGATATCTCAGGCATATGAGAGACCTTAGAGGAGTGGTGTGAAGAGACTTGGGGCCCCA	556
QY	796	TGGTGGCCGACGTGGTGGCTTCTACCCCCGGGCTGACGGGGTCAAGAGTGTGTCTTC	855
Db	557	TGGTGGCCGACGTGGTGGCTTCTACCCCCGGGCTGACGGGGTCAAGAGCTGTCTTC	616
QY	856	GGGTAGACCTTATGGGCTGCCTCGAGGGAGATGACCCGTGTACACGGGCCCCGTGG	915
Db	617	GGGTAGACCTTATGGGCTGCCTCGAGGGAGATGACCCGTGTGTACACGGGCCCCGTGG	676
QY	916	GGCAGCAATATTTATCTGAGGCGGTACCTCAACGACTCCACTATGAGAGACATA	975
Db	677	GGCAGCAATATTTATCTGAGGCGGTACCTCAACGACTCCACTATGAGAGACATA	736
QY	976	CCGTGGGGGACCTCAGTATGGGGGTGTGGGCCAGCTGGCAATGGTGTGTGGGGCTGG	1035
Db	737	CCGTGGGGGACCTCAGTATGGGGGTGTGGGCCAGCTGGCAATGGTGTGTGGGGCTGG	796
QY	1036	ATGACTTTAGGAAGAGTCAGAGAGTGGGGTCTGGCGAGGCTATGACTATGTGGGATGGA	1095
Db	797	ATGACTTTAGGAAGAGTCAGAGAGTGGGGTCTGGCGAGGCTATGACTATGTGGGATGGA	856
QY	1096	GCAACCAACGTTTCCAGTGGGTATGTGGAATGAGTTTGAAGTTTGAACCGGCTGAGGG	1155
Db	857	GCAACCAACGTTTCCAGTGGGTATGTGGAATGAGTTTGAAGTTTGAACCGGCTGAGGG	916
QY	1156	CCTTCACAGGCTATCAGGTCCAGTCACTGTAAACAATGACACGCGGGAGCGGTGCGCTG	1215
Db	917	CCTTCACAGGCTATCAGGTCCAGTCACTGTAAACAATGACACGCGGTGCGGTGCGCTG	976
QY	1216	GGGGGTGGAAATGTGCTTCGCGGCTGGGCGCTGCGATGGCGCTGGAGGGGAGACCATGC	1275
Db	977	GGGGGTGGAAATGTGCTTCGCGGCTGGGCGCTGCGATGGCGCTGGAGGGGAGACCATGC	1036
QY	1276	GCACAACCTAAGGGGGGCAACCTGGGGGAGACCCAGACCGGGGCTGTCTACAGTCCCCCTG	1335
Db	1037	GCACAACCTAAGGGGGGCAACCTGGGGGAGACCCAGACCCGGGCTGTCTACAGTCCCCCTG	1096
QY	1336	GGCGCGCTGTGGCTCGCTTCTGACAGTGGCGCTCTCTTTTCGGGGGCGCTGGTACTCT	1395
Db	1097	GGCGCGCGTGTGGCTCGCTTCTGACAGTGGCGCTCTCTTTTCGGGGGCGCTGGTACTCT	1156
QY	1396	TCACGGAATCTCCTTCATCTTGATGTGGTGAACAATTCCTCCGGCACTGGAGGACA	1455
Db	1157	TCACGGAATCTCCTTCATCTTGATGTGGTGAACAATTCCTCCGGCACTGGAGGACA	1216
QY	1456	CCTTCCCGGCAAGCCCTGTGTGGCGCGCTGGGCCAATCTCCCAACAATTCAGAGAGCTGG	1515
Db	1217	CCTTCCCGGCAAGCCCTGTGTGGCGCGCTGGGCCAATCTCCCAACAATTCAGAGAGCTGG	1276
QY	1516	AGCTGAGGCCAGAGGCGCAGACCGCTGGGCCAAGGCCAGAGGGAGCCCGACCGCATTC	1575
Db	1277	AGCTGAGGCCAGAGGCGCAGACCGCTGGGCCAAGGCCAGAGGGAGCCCGACCGCATTC	1336

[illegible]

Db	2399	TAGTTGGGAAAAATTTCACCATCAAAATCGCAACTTTGGATGAGCGGAACCTCTATG	2458
QY	2716	CAGGGGACTATTACCGTGTGAGGGGCGGGGCAATGCTGCCATCCGGCTGGAATGGCTGGG	2775
Db	2459	CTGGGACTATTACCGTGTGAGGGGCGGGGCAATGCTGCCATCCGGCTGGAATGGCTGGG	2518
QY	2776	AGTGCATCTCATGGGGGAAGTTCACGACTGCGAGTACGTGTGGGCTTTGGTGTGACCC	2835
Db	2519	AGTGCATCTCATGGGGGAAGTTCACGACTGCGAGTACGTGTGGGCTTTGGTGTGACCC	2578
QY	2836	TGTGGGAGGTCTGATATGCTGTGAGGGCCAGCCCTTTGGGACGTCAACGACGACGG	2895
Db	2579	TGTGGGAGGTCTGATATGCTGTGAGGGCCAGCCCTTTGGGACGTCAACGACGACGG	2638
QY	2896	TCATGGAAGCGGGGGGAGTCTCTCCGGGACACGGGCGGAGGTACCTGTCCGCCGC	2955
Db	2639	TCATGGAAGCGGGGGGAGTCTCTCCGGGACACGGGCGGAGGTACCTGTCCGCCGC	2698
QY	2956	CGCCTGCTGCCGACAGGGCTATATAGCTGTATGCTTGCTGGTGTGAGCGGGGAGTCTG	3015
Db	2699	CGCCTGCTGCCGACAGGGCTATATAGCTGTATGCTTGCTGGTGTGAGCGGGGAGTCTG	2758
QY	3016	AGCAGCAGCAACCCCTTTTCCACACTGATCGTGTCTGTGGCAGAGATCACTCAACAGG	3075
Db	2759	AGCAGCAGCAACCCCTTTTCCACACTGATCGTGTCTGTGGCAGAGATCACTCAACAGG	2818
QY	3076	TGTGATACACATCACTACGCTGCCCTCCCTCAAGGAGTATCAAGGGAACCAAGTACA	3135
Db	2819	TGTGATACACATCACTACGCTGCCCTCCCTCAAGGAGTATCAAGGGAACCAAGTACA	2878
QY	3136	CTAAACCAAGAGGACACATGCGACCTGTGCCCTTCCCTCCGACAGCCCATCACTCT	3195
Db	2879	CTAAACCAAGAGGACACATGCGACCTGTGCCCTTCCCTCCGACAGCCCATCACTCT	2938
QY	3196	AATAGAGCAATGTGAGTGTGAGGTGGGCTGGGGCCACCAAGGAGCTATGCCCTTCTC	3255
Db	2939	AATAGAGCAATGTGAGTGTGAGGTGGGCTGGGGCCACCAAGGAGCTATGCCCTTCTC	2958
QY	3256	CCCTTCTGGACACACTCTATGTCCCTGTGTTCTTCTCTAGAACCCCTGTGCG	3315
Db	2959	-----AAGACCCCTGTGCG 2972	
QY	3316	CCCAACCAAGGTGCTGTGTGAGATGGGATATCTCTCCACCCCTCTAGCAATCCTTGGGG	3375
Db	2973	CCCAACCAAGGTGCTGTGTGAGATGGGATATCTCTCCACCCCTCTAGCAATCCTTGGGG	3032
QY	3376	AAGGGTGGGAGAAATATAGATAGACACTGTGACATGCGCATTTGGAGACACTGGGCCC	3435
Db	3033	AAGGGTGGGAGAAATATAGATAGACACTGTGACATGCGCATTTGGAGACACTGGGCCC	3092
QY	3436	ACTGGACAACACTGATTTCTGGAGAGGTGGCTGG-CCCAAGCTTCTCTCCCTGTAC	3494
Db	3093	ACTGGACAACACTGATTTCTGGAGAGGTGGCTGG-CCCAAGCTTCTCTCCCTGTAC	3152
QY	3495	ACAATGACCCCACTGGCTGAGATATCTGGGGGTGAGAGGACAAGAAAGGAGAGAAATG	3554
Db	3153	ACAATGACCCCACTGGCTGAGATATCTGGGGGTGAGAGGACAAGAAAGGAGAGAAATG	3212
QY	3555	TTTCTTGTGCTGCTGTCTGTACTGTGTCTCACTTGGGCTTCTCTCTCATCACT	3614
Db	3213	TTTCTTGTGCTGCTGTCTGTACTGTGTCTCACTTGGGCTTCTCTCTCATCACT	3272
QY	3615	GAACAATGGAACCTGGGGGTAGCCCGGCGGAGCCCTAGTACACCCCACTCCCAATGG	3674
Db	3273	GAACAATGGAACCTGGGGGTAGCCCGGCGGAGCCCTAGTACACCCCACTCCCAATGG	3332
QY	3675	CAGTCTGTAGTAGAATCTCTAAGCCTATACGTTCTCTGTGAGTAAATATTGGGATT	3734
Db	3333	CAGTCTGTAGTAGAATCTCTAAGCCTATACGTTCTCTGTGAGTAAATATTGGGATT	3392
QY	3735	GGGGGGAAGAGGACCAACGGCCATAGCCTTGGGGTTGGACATCTCTAGTGTAGTGC	3794

Db	3393	GGGGGAAAAGAGGAGCAACGGCCCATAGCCTTGGGGTTGGACATCTGTAGTGTAGTGC	3452
QY	3795	CACATTGATTTTTCATATATACACTCTGGGCTTGTCACATTTTGGGGGAGAGACACAGAT	3854
Db	3453	CACATTGATTTTTCATATATACACTCTGGGCTTGTCACATTTTGGGGGAGAGACACAGAT	3512
QY	3855	TTTTCACATAATATATGACACTGAGTGGAGCAATTTTATCCCTGGACACTGGACAGTA	3914
Db	3513	TTTTCACATAATATATGACACTGAGTGGAGCAATTTTATCCCTGGACACTGGACAGTA	3572
QY	3915	ATAATAAGGTTGAGTTTTCACAAAAA	3953
Db	3573	ATAATAAGGTTGAGTTTTCACAAAAA	3611
RESULT 11			
LOCUS	AX268594	3554 bp	DNA
DEFINITION	Sequence 13 from Patent WO0175440.		
ACCESSION	AX268594		
VERSION	AX268594.1	GI:16541709	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and Pratt,J.Y.		
TITLE	Schizophrenia related genes		
JOURNAL	Patent: WO 0175440-A 13 11-OCT-2001;		
FEATURES	WELFIDE CORPORATION (JP)		
source	Location/Qualifiers		
	1..3554		
	/organism="Homo sapiens"		
	/db_xref="taxon:3606"		
BASE COUNT	682 a 1064 c 1065 g 743 t		
ORIGIN			
Query Match 85.4%; Score 3383.2; DB 6; Length 3554;			
Best Local Similarity 96.4%; Pred. No. 0; Mismatches 3; Indels 130; Gaps 3;			
QY	277	AGAGATGCTGCCCCCACCCTTAGGCCCCGAGGAGTACAGACTATGGAGCAGAGGCC	336
Db	2	AGAGATGCTGCCCCCACCCTTAGGCCCCGAGGAGTACAGACTATGGAGCAGAGGCC	61
QY	337	TGTCACTCTTACTGCTGCTCTTGGTGGCAAGTGAAGATGCTGACATGAAGGACATT	396
Db	62	TGTATCTTCTTACTGCTGCTCTTGGTGGCAAGTGAAGATGCTGACATGAAGGACATT	121
QY	397	TTGATCCCGCAATGCGCGATGCGCCGATGCGGAGCAGAGACCGGACATCCAGACAGT	456
Db	122	TGATTCGCGCAAGTGGCGGCTATGCCCTGGGCAATGACAGACCGGACATCCAGACAGT	181
QY	457	ACATCTCTGCTTCCAGCTCTGTGTAAGATTCCACTGCCGCCGACAGCAGAGTTGAGA	516
Db	182	ACATCTCTGCTTCCAGCTCTGTGTAAGATTCCACTGCCGCCGACAGCAGAGTTGAGA	241
QY	517	GCAGTGAAGGGAGTGGGCGCTGGGCGCCCGAGAGGTGGGTGTTCCAAAGAGAGAGT	576
Db	242	GCAGTGAAGGGAGTGGGCGCTGGGCGCCCGAGAGGTGGGTGTTCCAAAGAGAGAGT	301
QY	577	ACTTGCAAGTGAATCTACACAGCACTGACCTGAGGCTGTGTGGGACCCAGGAGGAGC	636
Db	302	ACTTGCAAGTGAATCTACACAGCACTGACCTGAGGCTGTGTGGGACCCAGGAGGAGC	361
QY	637	ATGGCGGGGGCGCTGGGCAAGAGATTCCCGGAGACTACCGGCTCTTATCCCGGGATG	696
Db	362	ATGGCGGGGGCGCTGGGCAAGAGATTCTCCCGGAGACTACCGGCTCTTATCCCGGGATG	421
QY	697	GTCGCCCTGTGATGGCTGGAAGAGACCGCTGGGGGTACAGAGTATCTTACGCAATAGG	756


```
|||||
Db 422 GTGCGCGCTGATGGGCTGGAAAGACCGCTGGGGTCAAGAGGTGATCTGAGGCAATGAGG 481
QY 757 ACCCTGAGGAGATGATGCTGGAAGACCTTGGGCCCCCATGTTGCCCACTGTTGCT 816
Db 482 ACCCTGAGGAGATGCTGGAAGACCTTGGGCCCCCATGTTGCCCACTGTTGCT 541
QY 817 TCTACCCCCGGGCTGACCGGGTCAATGATGCTGCTGGGGGTAGAGCTATAGGCTGCC 876
Db 542 TCTACCCCCGGGCTGACCGGGTCAATGATGCTGCTGGGGGTAGAGCTATAGGCTGCC 601
QY 877 TCTGAGGAGATGATGCTGCTTACACCGCCCTTGGGGGAGACAAATGATTTATCTG 936
Db 602 TCTGAGGAGATGATGCTGCTTACACCGCCCTTGGGGGAGACAAATGATTTATCTG 661
QY 937 AGCCCGTGTACTCAACGACTGCACTTACCTATGAGGACATACCGTGGCGGACTGACTATG 996
Db 662 AGCCCGTGTACTCAACGACTGCACTTACCTATGAGGACATACCGTGGCGGACTGACTATG 721
QY 997 GGGGCTGTGGGCGGAGCTGGAGATGCTGTGGGGCTGGATGACTTTAGGAAGTCAAG 1056
Db 722 GGGGCTGTGGGCGGAGCTGGAGATGCTGTGGGGCTGGATGACTTTAGGAAGTCAAG 781
QY 1057 AGCTCGGGTGTGGCGGAGCTATGACTATGAGGATGAGCAACACACACTTCTCCAGTG 1116
Db 782 AGCTCGGGTGTGGCGGAGCTATGACTATGAGGATGAGCAACACACACTTCTCCAGTG 841
QY 1117 GCTATGTGAGATGATGATTTGATTTGACCGGCTGAGGGCTTCCAGGCTATGCAAGTCC 1176
Db 842 GCTATGTGAGATGATGATTTGATTTGACCGGCTGAGGGCTTCCAGGCTATGCAAGTCC 901
QY 1177 ACTGTAAACAATGACACAGCTGGGAGCCGCTGCGCTGGGGGGTGAATGCTGCTCC 1236
Db 902 ACTGTAAACAATGACACAGCTGGGAGCCCGCTGCGCTGGGGGGTGAATGCTGCTCC 961
QY 1237 GCGGTGGCCCTGCAATGGCTTGGAGGGGAGCCCATGCGCCACAACCTTAGGGGGCAACC 1296
Db 962 GCGGTGGCCCTGCAATGGCTTGGAGGGGAGCCCATGCGCCACAACCTTAGGGGGCAACC 1021
QY 1297 TGGGGAGACCCGAGCGGGGCTGCTCAGTGGCCCCCTTGGGGCGGTGTGCTGCTTTC 1356
Db 1022 TGGGGAGACCCGAGCGGGGCTGCTCAGTGGCCCCCTTGGGGCGGTGTGCTGCTTTC 1081
QY 1357 TGCATGCGCGCTTCTCTTTGGGGGCGCTGTGCTACTCTTCAGCGAAATCTCTTCATCT 1416
Db 1082 TGCATGCGCGCTTCTCTTTGGGGGCGCTGTGCTACTCTTCAGCGAAATCTCTTCATCT 1141
QY 1417 CTGATGTGTGAACAATTCCTCTCCGCACTGGGAGGACCTTCCCGCCAGCCCTGTGT 1476
Db 1142 CTGATGTGTGAACAATTCCTCTCCGCACTGGGAGGACCTTCCCGCCAGCCCTGTGT 1201
QY 1477 GGGCGCCCTGGCCCACTCTCCCACTCAGACGTTGGAGCTGGAGCCAGAGCCAGC 1536
Db 1202 GGGCGCCCTGGCCCACTCTCCCACTCAGACGTTGGAGCTGGAGCCAGAGCCAGC 1261
QY 1537 AGCCCGTGGCAAGGCGGAGGAGCCGAGCCGACCTCTCTGCGCTGGGCTGGGGGCA 1596
Db 1262 AGCCCGTGGCAAGGCGGAGGAGCCGAGCCGACCTCTCTGCGCTGGGCTGGGGGCA 1321
QY 1597 TCAATCTGCTCTGCTGCTCATCATTTGCCCTCATGCTCTGGCGGCTGCACTGGCGAGG 1656
Db 1322 TCAATCTGCTCTGCTGCTCATCATTTGCCCTCATGCTCTGGCGGCTGCACTGGCGAGG 1381
QY 1657 TCTCTAGAGAGGCTGAGAGGAGGCTTGGAGAGAGAGCTGACGCTTACCTCTGTGCC 1716
Db 1382 TCTCTAGAGAGGCTGAGAGGAGGCTTGGAGAGAGAGCTGACGCTTACCTCTGTGCC 1441
QY 1717 CTGGGAGACTATCTCTATCAACAACGCCAGGCTTAGAGAGGACACCCCGTACCAAG 1776
Db 1442 CTGGGAGACTATCTCTATCAACAACGCCAGGCTTAGAGAGGACACCCCGTACCAAG 1501
QY 1777 AGCCCGGCGCTGTGGGAATCGGCCCACTCGCTCCCTGTGTCCCAATGGCTGTGCT 1836
|||||

Db 1502 AGCCCGGCGCTGTGGGAATCGGCCCACTCGGCTCCCTGTGTCCCAATGGCTCT --- 1557
QY 1837 TGTGCTCTTCCAAATCCAGCCTACCGGCTCTTCTTGGCCACTTACGGCCGCTCCCTCGAG 1896
Db 1558 ----- 1557
QY 1897 GCGCGGGCCCCCCCAACCCGCTGGGCCAACCACCAACCAAGGCTTACAGTGGGG 1956
Db 1558 -----GCTACAGTGGGG 1570
QY 1957 ACTATATGAGCCTGAGAAAGCCAGGCGCCCGTTTGCCTCCCACTCCCGAAGAGG 2016
Db 1571 ACTATATGAGCCTGAGAAAGCCAGGCGCCCGTTTGCCTCCCACTCCCGAAGAGG 1630
QY 2017 TCCCCATTATGCGGAGGCTGACATTTGTTACCTGAGGGGCTCAACGGGGCAACACT 2076
Db 1631 TCCCCATTATGCGGAGGCTGACATTTGTTACCTGAGGGGCTCAACGGGGCAACACT 1690
QY 2077 ATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2136
Db 1691 ATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1750
QY 2137 CTGATCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2196
Db 1751 CTGATCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1810
QY 2197 TGTGTGAGGTGCAAGACCCCTCAAGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2256
Db 1811 TGTGTGAGGTGCAAGACCCCTCAAGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1870
QY 2257 AGGGACACCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2316
Db 1871 AGGGACACCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1927
QY 2317 GCTTCTCTTGTCTTCCAGGAATGTTCTTCCAAAGAGGTGAAGATCATGTGAGGCTCA 2376
Db 1928 -----CAGGAATGATTTCTTCCAAAGAGGTGAAGATCATGTGAGGCTCA 1972
QY 2377 AGGACCCCAACATCATTTGGGCTGTGGGCGTGTGTGCAAGACACCCCTCTGATGA 2436
Db 1972 AGGACCCCAACATCATTTGGGCTGTGGGCGTGTGTGCAAGACACCCCTCTGATGA 2032
QY 2437 TTACTGACTACATGGAAGAGGCGGACCTTCAACCAATTTCTCAAGTGTCCCAACAGCTGAGG 2496
Db 2032 TTACTGACTACATGGAAGAGGCGGACCTTCAACCAATTTCTCAAGTGTCCCAACAGCTGAGG 2092
QY 2497 ACAAGGACGCGAGGGGCGCCCTGGGAGCGGGGAGGCTGGCGAGGGGCGCCACATCACT 2556
Db 2093 ACAAGGACGCGAGGGGCGCCCTGGGAGCGGGGAGGCTGGCGAGGGGCGCCACATCACT 2152
QY 2557 ACCCAATGCTGTGATGTGGAGCCAGATCGCTCCGGATGGCGCTATCTGAGCCACAC 2616
Db 2153 ACCCAATGCTGTGATGTGGAGCCAGATCGCTCCGGATGGCGCTATCTGAGCCACAC 2212
QY 2617 TCAACTTTGTATATGAGGAGCTGGGCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2676
Db 2213 TCAACTTTGTATGAGGAGGAGCTGGGCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2272
QY 2677 TCAAAATGCAAGACTTTGGCATGAGCGGAACTGTATGCGGGGAGCAATTAACGTGTGC 2736
Db 2273 TCAAAATGCAAGACTTTGGCATGAGCGGAACTGTATGCGGGGAGCAATTAACGTGTGC 2332
QY 2737 AGGGCGGGGAGTGTGCTGCCATCGGCTGATGGGCTGGGAGTGCATCTCAAGGGAGT 2796
Db 2333 AGGGCGGGGAGTGTGCTGCCATCGGCTGATGGGCTGGGAGTGCATCTCAAGGGAGT 2392
QY 2797 TCAGACTGCGAGTACGCTGTGGGCTTGTGTGACCTGTGTGGAGGCTGTGATGCTCT 2856
Db 2393 TCAGACTGCGAGTACGCTGTGGGCTTGTGTGACCTGTGTGGAGGCTGTGATGCTCT 2452
QY 2857 GTAGGCGGACCCCTTTGGGAGGCTCAACGAGGAGGAGTATGAGAGGCGGGGGAGT 2916
Db 2453 GTAGGCGGACCCCTTTGGGAGGCTCAACGAGGAGGAGTATGAGAGGCGGGGGAGT 2512
|||||
```

QY	2917	TCCTCCGGGACACAGGGCCGGAGGTTACCTGTCGCCGGCGCTGCTCCGCCAGGGCC	2917
Db	2513	TCCTCCGGGACACAGGGCCGGAGGTTACCTGTCGCCGGCGCTGCTCCGCCAGGGCC	2513
QY	2977	TATATGACCTGATGCTTCGGTGTGTGAGGCCGGGAGTCTGAGCAGGACACCCTTTTCC	2977
Db	2573	TATATGACCTGATGCTTCGGTGTGTGAGGCCGGGAGTCTGAGCAGGACACCCTTTTCC	2573
QY	3037	AGCTGCATCGGTTCTCTGGCAGAGGATGACATCAACACGGTGTGAATCACACATCCAGCTG	3037
Db	2633	AGCTGCATCGGTTCTCTGGCAGAGGATGACATCAACACGGTGTGAATCACACATCCAGCTG	2633
QY	3097	CCCCCTCCCTCAAGGAGATGATCCAGAGGGGAAGCCAGTACACTAAACAAGAGACACATG	3097
Db	2693	CCCCCTCCCTCAAGGAGATGATCCAGAGGGGAAGCCAGTACACTAAACAAGAGACACATG	2693
QY	3157	GCACCTCTGCCCTTCCCTCCCGACAGACCCTACCTGTAATAGAGCAGTGTAGACTGCA	3157
Db	2753	GCACCTCTGCCCTTCCCTCCCGACAGACCCTACCTGTAATAGAGCAGTGTAGACTGCA	2753
QY	3217	GATGGGCGTGGGCCACACCCAGGAGAGATGATGCCCTTCGCCCTTCTGTGACACACTGCA	3217
Db	2813	GATGGGCGTGGGCCACACCCAGGAGAGATGATGCCCTTCTGCCCTTCTGTGACACACTGCA	2813
QY	3277	TGTCCCTCTCTGTTCTTCTCTCTAGAAAGCCCTGTGCGCCACCCAGACTGGTCTGTGG	3277
Db	2873	TGTCCCTCTCTGTTCTTCTCTCTAGAAAGCCCTGTGCGCCACCCAGACTGGTCTGTGG	2873
QY	3337	ATGGGATTCCTCCACCCCTCTCTTACCCATCCCTTGGGGAAGGTTGGGGAAGATATAGC	3337
Db	2933	ATGGGATTCCTCCACCCCTCTCTTACCCATCCCTTGGGGAAGGTTGGGGAAGATATAGC	2933
QY	3397	ATAGACACTGTGACATGTGCCCATTTGGAGACACTGTGGGCCACCTGTGACACACTGATCTG	3397
Db	2993	ATAGACACTGTGACATGTGCCCATTTGGAGACACTGTGGGCCACCTGTGACACACTGATCTG	2993
QY	3457	GAGAGGTGGCTGGC - CCCACGTTCTCTCTCCCTGTACACACTGGACCCCACTGGCTGA	3457
Db	3053	GAGAGGTGGCTGGC - CCCACGTTCTCTCTCCCTGTACACACTGGACCCCACTGGCTGA	3053
QY	3516	GAATCTGGGGGTGAGAGGACAGAAAGAGAGAAATGTTCCCTGTGCCCTGCTCCTGT	3516
Db	3113	GAATCTGGGGGTGAGAGGACAGAAAGAGAGAAATGTTCCCTGTGCCCTGCTCCTGT	3113
QY	3576	ACTGTCTCTAGCTTGGGCTTCTCTCTCTCCATCACCCTGAAACACTGGACTGGGGGTA	3576
Db	3173	ACTGTCTCTAGCTTGGGCTTCTCTCTCTCCATCACCCTGAAACACTGGACTGGGGGTA	3173
QY	3636	GCCCCGCCGCCAGCCCTCAGTCAACCCCACTTCCCACTTGCAGTCTTGTAGCTAGACTTC	3636
Db	3233	GCCCCGCCGCCAGCCCTCAGTCAACCCCACTTCCCACTTGCAGTCTTGTAGCTAGACTTC	3233
QY	3696	TCTAAGCCTATACGTTCTGTGTGTGAGTAAATATTGGGATTGGGGGAAAGAGGAGCAAG	3696
Db	3293	TCTAAGCCTATACGTTCTGTGTGTGAGTAAATATTGGGATTGGGGGAAAGAGGAGCAAG	3293
QY	3756	GCCCATAGCCTTGGGGGTGGACATCTAAGTATAGCTCCACATGATTTTCTATATATC	3756
Db	3353	GCCCATAGCCTTGGGGGTGGACATCTAAGTATAGCTCCACATGATTTTCTATATATC	3353
QY	3816	ACTTGGGGTTGTACATTTTGGGGGAGAGACAGATTTTTCACATAATATATGAGC	3816
Db	3413	ACTTGGGGTTGTACATTTTGGGGGAGAGACAGATTTTTCACATAATATATGAGC	3413
QY	3876	TAGCTTAGGCAATTTTAAATCCCTGTGACATAGCAGGTAAATAAAGTTGATTTTCC	3876
Db	3473	TAGCTTAGGCAATTTTAAATCCCTGTGACATAGCAGGTAAATAAAGTTGATTTTCC	3473
QY	3936	ACAAAAAATTTTTTTTTT 3936	3936
Db	3533	ACAAAAAATTTTTTTTTT 3530	3533

[illegible]

```
Db 122 TTGATCTGCGCAAGTGCCTGATGCTCCGCGCATGCGAGACCGACATCCACAGACAGT 181
QY 457 ACATCTCTGCTTCCAGCTCCTGGTCAATTCACACTGCCCGCCACAGCAGGTTGAGA 516
Db 182 ACATCTCTGCTTCCAGCTCCTGGTCAATTCACACTGCCCGCCACAGCAGGTTGAGA 241
QY 517 GCATGACGGGGATGGGGCCGCGGCGAGGGTGGTTCCTCCAAAGAGAGAGAGT 576
Db 242 GCATGACGGGGATGGGGCCGCGGCGAGGGTGGTTCCTCCAAAGAGAGAGAGT 301
QY 577 ACTTGACGATGATCTCAACAGCCTCAGCTGTGGCTGTGGTGGGACCCAGGAGAGG 636
Db 302 ACTTGACGATGATCTCAACAGCCTCAGCTGTGGTGGTGGGACCCAGGAGAGG 361
QY 637 ATGCGGGGGGCTGGGAGAGAGGTTCTCCGAGACTACCGGCTGCTTACTCCGGAGT 696
Db 362 ATGCGGGGGGCTGGGAGAGAGGTTCTCCGAGACTACCGGCTGCTTACTCCGGAGT 421
QY 697 GTCGCCCTGATGGGCTGGAGAGACGCTGGGGTCAAGAGTGTCTCAGGCAATAGG 756
Db 422 GTGGCCCTGATGGGCTGGAGAGACGCTGGGGTCAAGAGTGTCTCAGGCAATAGG 481
QY 757 ACCCTGAGGAGTGTGCTGAAGAGACCTTGGCCCGCCATGTGTGCCGACTGGTGGCT 816
Db 482 ACCCTGAGGAGTGTGCTGAAGAGACCTTGGCCCGCCATGTGTGCCGACTGGTGGCT 541
QY 817 TCTACCCCGGGGCTGACCGGGGTATGATGTCTGTCTGCGGGTATAGCTTATGGCTGCC 876
Db 542 TCTACCCCGGGGCTGACCGGGGTATGATGTCTGTCTGCGGGTATAGCTTATGGCTGCC 601
QY 877 TCTGAGAGGATGAGCTCTGTCTTACACGCCCGCTGTGGGGAGACAAATATATATCTG 936
Db 602 TCTGAGAGGATGAGCTCTGTCTTACACGCCCGCTGTGGGGAGACAAATATATATCTG 661
QY 937 AGGCGCTGTACTCAAGCAGCTCCACCTATGACGAGCAGCATATACGTTGGGGAGCTGCAATG 996
Db 662 AGGCGCTGTACTCAAGCAGCTCCACCTATGACGAGCAGCATATACGTTGGGGAGCTGCAATG 721
QY 997 GGGGCTGGGGCCAGCTGGCAGATGTGTGGTGGGCTGGATGACTTATAGAGAGTACAGG 1056
Db 722 GGGGCTGGGGCCAGCTGGCAGATGTGTGGTGGGCTGGATGACTTATAGAGAGTACAGG 781
QY 1057 AGCTGGGGCTGGCCAGGCTATGACTATGTGGATGAGACCAACACAGCTTCCAGTG 1116
Db 782 AGCTGGGGCTGGCCAGGCTATGACTATGTGGATGAGACCAACACAGCTTCCAGTG 841
QY 1117 GCTATGTGAGATGAGATTGAGTTGACCGGCTGAGGGCTTCCAGGCTATGACAGTCC 1176
Db 842 GCTATGTGAGATGAGATTGAGTTGACCGGCTGAGGGCTTCCAGGCTATGACAGTCC 901
QY 1177 ACTGTAAACAATGACACAGCTGGAGCCGCTGTGCTGGCGGGTGAATGTGCTTCC 1236
Db 902 ACTGTAAACAATGACACAGCTGGAGCCGCTGTGCTGGCGGGTGAATGTGCTTCC 961
QY 1237 GGGGCTGGCCCTGGCATGGGCTGGGAGGGGAGCCCATGGCCCAACCTATAGGGGAGACC 1296
Db 962 GGGGCTGGCCCTGGCATGGGCTGGGAGGGGAGCCCATGGCCCAACCTATAGGGGAGACC 1021
QY 1297 TGGGGAGACCCAGAGCCCGGGGTGTCTCAGTGGCCCTTGGGGCGGTGTGGTCCGCTTTC 1356
Db 1022 TGGGGAGACCCAGAGCCCGGGGTGTCTCAGTGGCCCTTGGGGCGGTGTGGTCCGCTTTC 1081
QY 1357 TGCAGTGGCCCTTCTTGTGGGGGCGCTGTGTTACTTTCAGCGAATCTCTTCATCT 1416
Db 1082 TGCAGTGGCCCTTCTTGTGGGGGCGCTGTGTTACTTTCAGCGAATCTCTTCATCT 1141
QY 1417 CTGATGTGTTGAACAATCTCTCCGGGACCTGGAGAGCACTCCCGCCAGCCCTTGGT 1476
Db 1142 CTGATGTGTTGAACAATCTCTCCGGGACCTGGAGAGCACTCCCGCCAGCCCTTGGT 1201
QY 1477 GGCCTGCTGGCCCTCCCAACCTTACAGAGCTTGGAGCTGAGCCAGAGGCGACG 1536
|||||
Db 1202 GCGCCCTGGCCCACTCCCAACAATTCAGACAGCTTGAAGTGGAGCCCAAGAGCCAGC 1261
QY 1537 AGCCCGTGGCCAAAGCCGAGGGAGAGCCGACCCGACCTCTATCGGCTGCTGGTGGCCA 1596
Db 1262 AGCCCGTGGCCAAAGCCGAGGGAGAGCCGACCCGACCTCTATCGGCTGCTGGTGGCCA 1321
QY 1597 TCATCTGCTCTCTGCTCATATTTGCTCTCATGCTGTCTGGGGCTCTCACTGGCGAGGC 1656
Db 1322 TCATCTGCTCTCTGCTCATATTTGCTCTCATGCTGTCTGGGGCTCTCACTGGCGAGGC 1381
QY 1657 TCTCCACCAAGGCTGAGACGGAGGGTGTGGAAGAGAGGATGAGGCTTACCTCTGTGTC 1716
Db 1382 TCTCCACCAAGGCTGAGACGGAGGGTGTGGAAGAGAGGATGAGGCTTACCTCTGTGTC 1441
QY 1717 CTGGGAGACTATCTCATCAACAACCCGACAGCTCTAGAGAGCCACCCCGTACAGG 1776
Db 1442 CTGGGAGACTATCTCATCAACAACCCGACAGCTCTAGAGAGCCACCCCGTACAGG 1501
QY 1777 AGCCCGGCTCTGTGGGATTCGCGCCACTCCGCTCTGTCTGTCCTCATGTGCTGCT 1836
Db 1502 AGCCCGGCTCTGTGGGATTCGCGCCACTCCGCTCTGTCTGTCCTCATGTGCTGCT --- 1557
QY 1837 TGCTGCTCTCAATCCAGCCTACCGCTCTTGTGGCACTTAAGCCCGCTCCCTCGAG 1896
Db 1558 ----- 1557
QY 1897 GCGCCGCGCCCGCCACACCGCGCTGGGCAAAACCACACACCCAGGCTTACAGTGGG 1956
Db 1558 -----GCTTAAGTGGG 1570
QY 1957 ACTATATGAGGCTGAGAAACCGAGCGCCCGCTTGTGCCCCACCTCCCAAGACG 2016
Db 1571 ACTATATGAGGCTGAGAAACCGAGCGCCCGCTTGTGCCCCACCTCCCAAGACG 1630
QY 2017 TCCCGCATATGCGAGAGGCTGACATTTGTACCTGCGAGGGCGTACCGGGGGAGAACCT 2076
Db 1631 TCCCGCATATGCGAGAGGCTGACATTTGTACCTGCGAGGGCGTACCGGGGGAGAACCT 1690
QY 2077 ATGCTGTGCTGACATGCCCCCAGGGGAGTGGGGATGGGCCCGCCAGAGTGGATTCC 2136
Db 1691 ATGCTGTGCTGACATGCCCCCAGGGGAGTGGGGATGGGGCGCCCGCAGAGTGGATTCC 1750
QY 2137 CTGATCTGACATCCGCTTAAAGAGAACTTGGCGAGGGCCAGTTGGGGAGTGCACC 2196
Db 1751 CTGATCTGACATCCGCTTAAAGAGAACTTGGCGAGGGCCAGTTGGGGAGTGCACC 1810
QY 2197 TGTGTGAGTGCAGACCGCCCAAGATGTGTCAGTCTTATTTCCCGCTTAATGTGCGTA 2256
Db 1811 TGTGTGAGTGCAGACCGCCCAAGATGTGTCAGTCTTATTTCCCGCTTAATGTGCGTA 1870
QY 2257 AGGAGACACCTTGTGTGATGTCAGTCAAGTCTTACGGCCAGATGCGACCAAGAAATGCA 2316
Db 1871 AGGAGACACCTTGTGTGATGTCAGTCAAGTCTTACGGCCAGATGCGACCAAGAAATG --- 1927
QY 2317 GCTTCTCTTGTCTCTCAGAGATGATTTCTGAAAGAGTGAAGATCATGTGAGGCTCA 2376
Db 1928 -----CCAGGAATGATTTCTGAAAGAGTGAAGATCATGTGAGGCTCA 1972
QY 2377 AGGAGCCCAACATCATTTGGGCTGTGGGGGTGTGTGAGAGAGAGCCCGCTCGATGA 2436
Db 1973 AGGAGCCCAACATCATTTGGGCTGTGGGGGTGTGTGAGAGAGAGCCCGCTCGATGA 2032
QY 2437 TTAAGTACTATGAGAGAGGAGCTCAACAGTCTCTCAGTGGCCACAGCTGAGAG 2496
Db 2033 TTAAGTACTATGAGAGAGGAGAGCTCAACAGTCTCTCAGTGGCCACAGCTGAGAG 2092
QY 2497 ACAAGGACCCAGAGGGGCGCTGGGAGGCGGAGGCTGCGAGGGGCCACATCACT 2556
Db 2093 ACAAGGACCCAGAGGGGCGCTGGGAGGCGGAGGCTGCGAGGGGCCACATCACT 2152
QY 2557 ACCCAATGCTGTGATGAGAGGAGGCGGAGGCGGCTGGGAGGAGGAGGAGGAGGAGG 2616
Db 2153 ACCCAATGCTGTGATGAGAGGAGGCGGAGGCGGCTGGGAGGAGGAGGAGGAGGAGGAGG 2212
```

QY 2617 TCAACTTGTACATCGGAGCTGGCCACGCGGAACTGCCAGTGGGGGAAATTTTCACCA 2676
 DB 2213 TCAACTTGTACATCGGAGCTGGCCACGCGGAACTGCCAGTGGGGGAAATTTTCACCA 2272
 QY 2677 TCAAAATCGCAGACTTGGCATGAGCCGGAACCTCTATCTGGGAGCTATTAACCGTGTGC 2736
 DB 2273 TCAAAATCGCAGACTTGGCATGAGCCGGAACCTCTATCTGGGAGCTATTAACCGTGTGC 2332
 QY 2737 AGGGCCGGGAGTGTGCCATCCGCTGATGGCCCTGGGAGTGCATCCATGAGGGGAACT 2796
 DB 2333 AGGGCCGGGAGTGTGCCATCCGCTGATGGCCCTGGGAGTGCATCCATGAGGGGAACT 2392
 QY 2797 TCAAGCATCGAGTACGTGTGGGCTTTGGTGTGACCTGTGGGAGTGTGATGCTCT 2856
 DB 2393 TCAAGCATCGAGTACGTGTGGGCTTTGGTGTGACCTGTGGGAGTGTGATGCTCT 2452
 QY 2857 GTAGGGCCAGCCCTTTGGGAGCTCAGCAGCAGCAGAGTCAATCGAAGACGGGGGAGT 2916
 DB 2453 GTAGGGCCAGCCCTTTGGGAGCTCAGCAGCAGCAGAGTCAATCGAAGACGGGGGAGT 2512
 QY 2917 TCTTCCGGGAGCAGGCGGAGGTGTACCTGTCCCGGCGGCTGCTCCGAGGGGC 2976
 DB 2513 TCTTCCGGGAGCAGGCGGAGGTGTACCTGTCCCGGCGGCTGCTCCGAGGGGC 2572
 QY 2977 TATATGAGCTGATGCTTCCGCTGTGGAGCCGGGAGTCTGAGCAGCAGCAGCTTTTCC 3036
 DB 2573 TATATGAGCTGATGCTTCCGCTGTGGAGCCGGGAGTCTGAGCAGCAGCAGCTTTTCC 2632
 QY 3037 AACCTGATGGGTCTCTCGGAGAGAGTGCATCAACAGGTGTGAATCACACATCCAGCTG 3096
 DB 2633 AACCTGATGGGTCTCTCGGAGAGAGTGCATCAACAGGTGTGAATCACACATCCAGCTG 2692
 QY 3097 CCCCTCCCTCAGAGGAGTATCCAGGGGAAAGCCAGTACACTAAACAGAGACAAATG 3156
 DB 2693 CCCCTCCCTCAGAGGAGTATCCAGGGGAAAGCCAGTACACTAAACAGAGACAAATG 2752
 QY 3157 GCACCTGTGCTTCCCTCCCTCCGAGACGCCATCACCTTAATAGAGCAGTACAGCTGA 3216
 DB 2753 GCACCTGTGCTTCCCTCCCTCCGAGACGCCATCACCTTAATAGAGCAGTACAGCTGA 2812
 QY 3217 GGTGGGCTGGGCGCAACCCAGGAGTGAATGCCCCCTTCTGACACACTCTCA 3276
 DB 2813 GGTGGGCTGGGCGCAACCCAGGAGTGAATGCCCCCTTCTGACACACTCTCA 2872
 QY 3277 TGTCCCTCTCTCTCTCTCTCTAGAAAGCCCTGTGCGCCACCAAGTGTCTCTG 3336
 DB 2873 TGTCCCTCTCTCTCTCTCTCTAGAAAGCCCTGTGCGCCACCAAGTGTCTCTG 2932
 QY 3337 ATGGGATCTCTCAACCTCTCTAGCCATCCCTTGGGAGAGGTGGGAGAAATATAG 3396
 DB 2933 ATGGGATCTCTCAACCTCTCTAGCCATCCCTTGGGAGAGGTGGGAGAAATATAG 2992
 QY 3397 ATAGACATCGGAGATGGCCATGAGACACATGAGGCCCCCAGTGCACATGATTCCTG 3456
 DB 2993 ATAGACATCGGAGATGGCCATGAGACACATGAGGCCCCCAGTGCACATGATTCCTG 3052
 QY 3457 GAGAGGTGGCTGCG-CCCCAGCTCTCTCTCTCTCAACACTGAGCCCACTGGCTGA 3515
 DB 3053 GAGAGGTGGCTGCGCCCGCCAGTCTCTCTCTCTCAACACTGAGCCCACTGGCTGA 3112
 QY 3516 GAATGTGGGGGTGAGAGAGACAAGAGAGAAATGTTCTTGTGCTGCTCTCTG 3575
 DB 3113 GAATGTGGGGGTGAGAGAGACAAGAGAGAAATGTTCTTGTGCTGCTCTCTG 3172
 QY 3576 ACTTGTCTCAAGCTTGGGCTTCTCTCTCATATCACTGAACACTGAGCTGGGGTA 3635
 DB 3173 ACTTGTCTCAAGCTTGGGCTTCTCTCTCATATCACTGAACACTGAGCTGGGGTA 3232
 QY 3636 GCGCCGCGCCAGCTCTAGTACCCCACTTCCACTTGCAGTCTGTAGTATAGTATC 3695
 DB 3233 GCGCCGCGCCAGCTCTAGTACCCCACTTCCACTTGCAGTCTGTAGTATAGTATC 3292

QY 3696 TCTAAGCCCTATACGTTTCTGTGAGTAATATGGGATGGGGGAAAGAGGAGCAACG 3755
 DB 3293 TCTAAGCCCTATACGTTTCTGTGAGTAATATGGGATGGGGGAAAGAGGAGCAACG 3352
 QY 3756 GCCATAGCCCTTGGGCTGGAGCATCTAGTGTAGCTGCACATGATTTTCTATATC 3815
 DB 3353 GCCATAGCCCTTGGGCTGGAGCATCTAGTGTAGCTGCACATGATTTTCTATATC 3412
 QY 3816 ACTTGGGGTGTACATTTTGGGGGAGAGACAGATTTTACACTAATATATGAC 3875
 DB 3413 ACTTGGGGTGTACATTTTGGGGGAGAGACAGATTTTACACTAATATATGAC 3472
 QY 3876 TAGCTTGAAGCAATTTTATCCCTGACACTAGCAGGTATATATAGGTATGTTTCC 3935
 DB 3473 TAGCTTGAAGCAATTTTATCCCTGACACTAGCAGGTATATATAGGTATGTTTCC 3532
 QY 3936 ACAAACAAAAA 3953
 DB 3533 ACAAACAAAAA 3550

RESULT 13

HSRETYK1

LOCUS HSRETYK1 3841 bp mRNA linear PRI 20-APR-1995

DEFINITION H.sapiens EDDR1 gene for receptor tyrosine kinase.

ACCESSION Z29093

VERSION Z29093.1 GI:732799

KEYWORDS receptor tyrosine kinase.

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Laval,S., Butler,R., Shelling,A.N., Hanby,A.M., Poulson,R. and
Ganesan,I.S.

Isolation and characterization of an epithelial-specific receptor
tyrosine kinase from an ovarian cancer cell line

Cell Growth Differ. 5 (11), 1173-1183 (1994)

REFERENCE

AUTHORS

Shelling,A.N., Butler,R., Jones,T., Laval,S., Boyle,J.M. and
Ganesan,I.S.

Localization of an epithelial-specific receptor kinase (EDR1) to
chromosome 6q16

Genomics 25 (2), 584-587 (1995)

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

Direct Submision
Submitted (17-DEC-1993) Claude Kedinger, CNRS Laboratoire de
genetique moleculaire-U184, INSERM, 11, rue Humann, Strasbourg,
Alsace, 67085 cedex, FRANCE

JOURNAL

FEATURES

source

1. 3841
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RTK6"

/cell_line="SKOV-3"
/cell_type="Epithelial cell"
/tissue_type="Ovary"
/clone_lib="PKS"
/dev_stage="Adult"

336..423
/note="putative signal peptide"
337..2967
/gene="EDDR1"

337..2967
/gene="EDDR1"
/gene="EDDR1"
/standard_name="epithelial discoidin domain receptor"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="CAA82335.1"

Db	1922	TCGCCCAATTATGCGGAGGCTGACATATGTTAACTCGAGGGGCTCAACGGGGCAACACT	1961
QY	2077	ATGCTGTGCTGCACTGCTGCCCCCAAGGGGACATGCGGGAGTGGCCCCCAGATGATATTTCC	2136
Db	1982	ATGCTGTGCTGCACTGCTGCCCCCAAGGGGACATGCGGGAGTGGCCCCCAGATGATATTTCC	2041
QY	2137	CTGANTCCGACATCCGGTTCTTAAAGGAAACCTTGGCGAGGGCCAGTTTGGGAGGTGCAC	2186
Db	2042	CTGATCTCGACATCCGGTTCTTAAAGGAAACCTTGGCGAGGGCCAGTTTGGGAGGTGCAC	2101
QY	2197	TGTGTGAGGTGACAGGCCCCCAAGATCTGGTCAAGTCTTATTTCCCTTAATGTGCTCA	2256
Db	2102	TGTGTGAGGTGACAGGCCCCCAAGATCTGGTCAAGTCTTATTTCCCTTAATGTGCTCA	2151
QY	2257	AGGACACCCCTTTGCTGTGATGCTGTCAAGATCTTACGGCCAGATGCCAACAAATGCCA	2316
Db	2162	AGGACACCCCTTTGCTGTGATGCTGTCAAGATCTTACGGCCAGATGCCAACAAATGCCA	2218
QY	2317	GCTTCTCCTTGTCTCCAGGAATGATTTCTGAAAGGTGAAGTCAATGTGAGGCTCA	2376
Db	2219	-----CCAGGAATGATTTCTGAAAGGTGAAGTCAATGTGAGGCTCA	2263
QY	2377	AGGACCCCAATCATATTCGGCTGCTGCGGGGTGATGTGAGGACGACACCCCTTCGACATGA	2436
Db	2264	AGGACCCCAATCATATTCGGCTGCTGCGGGGTGATGTGAGGACGACACCCCTTCGACATGA	2333
QY	2437	TTACTGACTACATGAGAAAGGCGGACCTCAACAGTTCTCAGTCCCAACAGGTGAGG	2496
Db	2334	TTACTGACTACATGAGAAAGGCGGACCTCAACAGTTCTCAGTCCCAACAGGTGAGG	2383
QY	2497	ACAAAGGACGCCGAGGGGGCCCTGGGGACGGGACGGGCTGCGACAGGGGCCACATCACT	2556
Db	2384	ACAAAGGACGCCGAGGGGGCCCTGGGGACGGGACGGGCTGCGACAGGGGCCACATCACT	2443
QY	2557	ACCCAAATGCTGCGAATGATGGGACGCCCAATGCGCTCGCGCATGCGCTATGTGGCCACAC	2616
Db	2444	ACCCAAATGCTGCTGCAATGATGGGACGCCCAATGCGCTCGCGCATGCGCTATGTGGCCACAC	2503
QY	2617	TCAACTTTGACATCGGGACCTGGCCACCGGACCTGCCTAGTTGGGGAATAATTTCACA	2676
Db	2504	TCAACTTTGACATCGGGACCTGGCCACCGGACCTGCCTAGTTGGGGAATAATTTCACA	2563
QY	2677	TCAAAATCGGACATTTGGCATATGACCGGACCTCTATGCTGGGACATTAATACGTGTC	2736
Db	2564	TCAAAATCGGACATTTGGCATATGACCGGACCTCTATGCTGGGACATTAATACGTGTC	2623
QY	2737	AGGGCGGGGACATGTCGCCCATCCGCTGGATGGGCTGGGAGTGCATCTCATGGGGAGT	2796
Db	2624	AGGGCGGGGACATGTCGCCCATCCGCTGGATGGGCTGGGAGTGCATCTCATGGGGAGT	2683
QY	2797	TCAAGATGCGGATGACGTGTGGGGCTTTGGTGTACACCTGTGGGAGGTGTGATGCTCT	2856
Db	2684	TCAAGATGCGGATGACGTGTGGGGCTTTGGTGTACACCTGTGGGAGGTGTGATGCTCT	2743
QY	2857	GTAAGGCCACAGCCCTTTGGGACAGCTCACCGGACGACAGTATCGAGAGCGGGGGAGT	2916
Db	2744	GTAAGGCCACAGCCCTTTGGGACAGCTCACCGGACGACAGTATCGAGAGCGGGGGAGT	2803
QY	2917	TCTTCCGGGACACGGGGCCGGGACAGGTATCTCTCCCCGCCCTGCTGCTGCCGAGGGCC	2976
Db	2804	TCTTCCGGGACACGGGGCCGGGACAGGTATCTCTCCCCGCCCTGCTGCTGCCGAGGGCC	2863
QY	2977	TATATGAGCGATGCTCGGTGCTGTGGAGCCGGGAGTCTGACAGAGGACACCTTTTCCC	3036
Db	2864	TATATGAGCGATGCTCGGTGCTGTGGAGCCGGGAGTCTGACAGAGGACACCTTTTCCC	2923
QY	3037	AGCTGCATCGGTTCTGTGGGACAGAGTGCATCAACAGGTGTGATCAACATCAACTG	3096
Db	2924	AGCTGCATCGGTTCTGTGGGACAGAGTGCATCAACAGGTGTGATCAACATCAACTG	2983
QY	3097	CCCCCTCCCTCAGGAGATGATCCAGGGGAAAGCATGTGACACTTAAACAAAGAGACACATG	3156
Db	2984	CCCCCTCCCTCAGGAGACGATCCAGGGGAAAGCATGTGACACTTAAACAAAGAGACACATG	3043

QY	3157	GCACCTGACCCCTTCCCTCCCGGACAGCCCATACCTCTTAATAAGAGGCACTGACCTGCA	3216
Db	3044	GCACCTCTGCCCCCTCCCTCCCGGACAGCCCATACCTCTTAATAAGAGGCACTGACCTGCA	3103
QY	3217	GGTGGGCTGGGGCCACCCAGGAGGCTGATGCCCCCTTCTCCCTTCTGAGACACTGTCA	3276
Db	3104	GGTGGGCTGGGGCCACCCAGGAGGCTGATGCCCCCTTCTCCCTTCTGAGACACTGTCA	3163
QY	3277	TGTCCCTTCTGTTCTTCTTCTTCTTAAGA--CCCTGTGCCCCACCCAGCTGTCTGT	3334
Db	3164	TGTCCCTTCTGTTCTTCTTCTTCTTAAGA--CCCTGTGCCCCACCCAGCTGTCTGT	3223
QY	3335	GGATGGATGCTCTCCACCCCTCTCTAGCATCCCTTGGGGAAAGGTGGGGGAATAATA	3394
Db	3224	GGATGGATGCTCTCTCACCCCTCTCTAGCATCCCTTGGGGAAAGGTGGGGGAATAATA	3283
QY	3395	GGATGAGACACTGGACATGGCCCATTTGAGACACTGTGGGCCCTGAGACACTGATTC	3454
Db	3284	GGATGAGACACTGGACATGGCCCATTTGAGACACTGTGGGCCCTGAGACACTGATTC	3343
QY	3455	TGGAGAGGTGGCTGCG--CCCAAGCTTCTCTCTCCCTGTACACACTGGAACCCACTGGCT	3513
Db	3344	TGGAGAGGTGGCTGCG--CCCAAGCTTCTCTCTCCCTGTACACACTGGAACCCACTGGCT	3403
QY	3514	GAGATCTGGGGGCTGAGAGGACAGAAAGAGAGAGAAATGTTCTCTTGTGCTCTCT	3573
Db	3404	GAGATCTGGGGGCTGAGAGGACAGAAAGAGAGAGAAATGTTCTCTTGTGCTCTCT	3463
QY	3574	GTACTTGTCTCAGCTTGGGCTTCTCTCTCCATCACACTGAAACACTGGACCTGGGG	3633
Db	3464	GTACTTGTCTCAGCTTGGGCTTCTCTCTCCATCACACTGAAACACTGGACCTGGGG	3523
QY	3634	TAGCCCCGCCCCAGCCCTCAGTACACCCCACTTCCCACTTGCACTGTGTAGCTAGAACT	3693
Db	3524	TAGCCCCGCCCCAGCCCTCAGTACACCCCACTTCCCACTTGCACTGTGTAGCTAGAACT	3583
QY	3694	TCTCTAACCTATACCTTCTGTGGAGTAATAATTTGGGATTGGGGGAAAGAGGAGCA	3753
Db	3584	TCTCTAACCTATACCTTCTGTGGAGTAATAATTTGGGATTGGGGGAAAGAGGAGCA	3643
QY	3754	CGGCCCATAGCCCTGGGGTTGGACATCTCTAGTAGCTGCACATTTATTTTGTATTA	3813
Db	3644	CGGCCCATAGCCCTGGGGTTGGACATCTCTAGTAGCTGCACATTTATTTTGTATTA	3703
QY	3814	TCACTTGGGGTTTGTACATTTTGGGGGAGAGACACAGATTTTACATAATATATGA	3873
Db	3704	TCACTTGGGGTTTGTACATTTTGGGGGAGAGACACAGATTTTACATAATATATGA	3763
QY	3874	CCTAGCTGAGGCAATTTAATCCCTCCTCCTAGCAGCTAATAATAAGTGTAGTTT	3933
Db	3764	CCTAGCTGAGGCAATTTAATCCCTCCTCCTAGCAGCTAATAATAAGTGTAGTTT	3823
QY	3934	CCACAAAAAATAAAAAA 3951	
Db	3824	CCACAAAAAATAAAAAA 3841	
RESULT	14		
LOCUS	HUMCKA		
DEFINITION	Homo sapiens Cak receptor kinase mRNA, complete cds.		
VERSION	L57508.1 GI:1160924		
KEYWORDS	receptor kinase.		
SOURCE	Homo sapiens lung cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.		
AUTHORS	Perez, J. L., Jling, S. O. and Wong, T. W.		
TITLE	Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines		

D	b	1502	TGCTGTGGCGGCTGCACCTGGCGGAGGCTCTCTGACAGAGGCTGAACGAGGCTGTGGAG	1561
Q	y	1690	AGGAGCTACGCGTTACCTCTCTGTCTCCCTGGGACACTATCTCATCAACACGCCGAC	1749
D	b	1562	AGGAGCTAGAGGTTACACTCTCTGTCTCCCTGGGACACTATCTCATCAACACGCCGAC	1621
Q	y	1750	GTCTAGAGAGCACACCCCGTACCAAGAGCCCGGCTGTGGGAATCCGCCACTCCG	1809
D	b	1622	GTCCTAGAGAGCACACCCCGTACCAAGAGCCCGGCTGTGGGAATCCGCCACTCCG	1681
Q	y	1810	CTCCCTGTGTCCCAATGGCTCTGTGCTGTCTCAATCCAGCTACCGCTCTCTTC	1868
D	b	1682	CTCCCTGTGTCCCAATGGCTCTCTGTGCTGTCTCAATCCAGCTACCGCTCTCTTC	1704
Q	y	1870	TGGCCACTTACGCGCGTCCCTTCGAGAGCGCGCGCCGCCACACCGCGCTGGGCCAAC	1929
D	b	1705	-----1-----	1704
Q	y	1930	CCACCAACACCAGGCTTACAGTGGGAGCTATATGAGGCTGAGAGCCAGCGCCCGC	1989
D	b	1705	-----GCTTACAGTGGGAGCTATATGAGGCTGAGAGCCAGCGCCCGC	1750
Q	y	1990	TTTCGCCCCCACCCTCCCAACAACAGGCTCCCATTTATCGGAGGCTGACATTGTATCC	2049
D	b	1751	TTTCGCCCCCACCCTCCCAACAACAGGCTCCCATTTATCGGAGGCTGACATTGTATCC	1810
Q	y	2050	TGCAGGGGCTACCGGGGGGACACCTATGCTGTGCTGCATCGGCCCAAGGGGACGCG	2109
D	b	1811	TGCAGGGGCTACCGGGGGGACACCTATGCTGTGCTGCATCGGCCCAAGGGGACGCG	1870
Q	y	2110	GGGATGGGCCCCCAGTAGTGATTTCCCTCGATCTGCATCCGCTTCAAGGAGAACTTG	2169
D	b	1871	GGGATGGGCCCCCAGTAGTGATTTCCCTCGATCTGCATCCGCTTCAAGGAGAACTTG	1930
Q	y	2170	GCAGGGGCACTTGGGGAGGAGTCACTGTGTGAGTGCACAGCCCTCAAGTGTGTCA	2229
D	b	1931	GCAGGGGCACTTGGGGAGGAGTCACTGTGTGAGTGCACAGCCCTCAAGTGTGTCA	1990
Q	y	2230	GTCCTGATTTCCCTTAATGTGCTGTAAGGACACCTTGTGTGAGTGTGCAAGATCT	2289
D	b	1991	GTCCTGATTTCCCTTAATGTGCTGTAAGGAGACCTTGTGTGAGTGTGCAAGATCT	2050
Q	y	2290	TACGGCAGATGCCACCAAGAATGCCAGCTTCTCTGTTCACAGAGATGTTTCTCGA	2349
D	b	2051	TACGGCAGATGCCACCAAGAATG-----CAAGAGATGTTTCTCGA	2092
Q	y	2350	AAGAGGTGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTTGGCTGTGGGCGTGT	2409
D	b	2093	AAGAGGTGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTTGGCTGTGGGCGTGT	2152
Q	y	2410	GTCGACAGAGACACCCCTGTGATATTAATGACATACATGAGAACGGGCACTCAAC	2469
D	b	2153	GTCGACAGAGACACCCCTGTGATATTAATGACATACATGAGAACGGGCACTCAAC	2212
Q	y	2470	AGTTCTCAGTGCACACACAGCTGGAGAACAGGACCGGAGGGGCGCTGTGGGACGGC	2529
D	b	2213	AGTTCTCAGTGCACACACAGCTGGAGAACAGGACCGGAGGGGCGCTGTGGGACGGC	2272
Q	y	2530	AGGCTGGCGACAGGGGCCACCATATGCTACCCAAATGCTGTCATGTGGCACCCAGATCG	2589
D	b	2273	AGGCTGGCGACAGGGGCCACCATATGCTACCCAAATGCTGTCATGTGGCACCCAGATCG	2332
Q	y	2590	CCCTCGGCAATGCGGTATGCTGGGACACACTAATTTGTACATGGGAGACTGGGCAACGGGA	2649
D	b	2333	CCCTCGGCAATGCGGTATGCTGGGACACACTAATTTGTACATGGGAGACTGGGCAACGGGA	2392
Q	y	2650	ACTGCTAGTTGGGAAAAATTTCCACATCAAAATGCGAGACTTTGGCATGAGCCGGAAC	2709
D	b	2393	ACTGCTAGTTGGGAAAAATTTCCACATCAAAATGCGAGACTTTGGCATGAGCCGGAAC	2452
Q	y	2710	TCTATGCTGGGAGCTATTTACCTGTGTGACAGGCGCGGCACTGCTGCCATCCGCTGATGG	2769
D	b	2453	TCTATGCTGGGAGCTATTTACCTGTGTGACAGGCGCGGCACTGCTGCCATCCGCTGATGG	2512

[illegible]

[illegible]

[illegible]

Db	2085	ATG-----	-----CCAGGAAATATTTCTGAAGAGGGATGAAGATCATGTAC	2126
Qy	2371	GGCTCAAGAGACCCCAACATCATTTGGCTGGGGCGGTGTGTGACAGACACCCCTCT		2430
Db	2127	GGCTGAAGAGACCCCAACATCATTCGGGCTCCTGGGTGTGTGTGTGACAGATGACCCCTCT		2186
Qy	2431	GCATATATTACTGACTACATGAGAGACGGCACCTCAACAGTTCTCTAGTCCCAACAGC		2490
Db	2187	GCATATATCAAGACTACATGTAGAGAACGGCAGTCATGAAACAGTTCTCTAGTCCCAACAGC		2248
Qy	2491	TGGAGACAAAGGACCGAGGGGGCCCTGGGGAGCGGAGGGGTGGCGAGGGGGCCACCA		2550
Db	2247	TGGAAACAAAGGCCACTCAGGGGCTCTCTGTGGGACACAGATGTGACCAAGGGGCCACAA		2306
Qy	2551	TCAGCTACCAATGCTGTGATGTGGACCCAGATTCGGCTTCGGGCATGCCATCTCTGG		2610
Db	2307	TCAGCTACCCATGCTGTGATACATGTGGGGGCCAGATTCGGCTTCGGCATGCTTATCTCG		2366
Qy	2611	CCACACTCAACTTTGTATCATTCGGGACCTGGGCCACGGGGAACTGCCATAGTTGGGGAAATT		2670
Db	2367	CCACCTCAACTTTGTGTGATGGGACCTGGGCCACCGGAACTGCTGTGTGGGGAAATT		2428
Qy	2671	TCACCATCAAAATGCGAGACTTTTGGCATGAGCCGGAACCTCTATGCTGGGAGCTATTAC		2730
Db	2427	TCACCATCAAAATGCGCGAGCTTTGGCATGAGCCGGAATCTCTACGCTGGGGATTTATTAC		2486
Qy	2731	GTGTCAAGGGCCGGGCAATGCTGCCATCCGCTGTGATGGCTTGGAGTGCATCTCTATGG		2790
Db	2487	GTGTCCAGGGCCGGGCGGTGTGTGCCATCAAGGTGATGGCTTGGAGTGCATCTCTATGG		2546
Qy	2791	GGAAATTCACACTGCGAGTGTGACCTGTGGGACCTTTGGTGTGACCCCTGGAGGTGTCTGA		2850
Db	2547	GGAAATTCACAAAGCAAGCATGTAGCTTTGGGCTTCGGAGTGAACCTGTGGAGGTGTCTGA		2606
Qy	2851	TGCTCTGTAGGGCCCCAGCCCTTTTGGCATCTCAACGACAGCATGTCAAGAACCGG		2910
Db	2607	TGCTCTGTAGAGTCCCAAGCCCTTTTGGCAGCTTCAAGATGACAGGTTATTCGAAATTCGG		2666
Qy	2911	GGGAGTTTTCCTGGGAGACAGGGCCGGGAGGTGTAACGTTCGGGCGCCGCTGACTACCGC		2970
Db	2667	GGGAGTTTTCCTAGGAGACAGGGCCGGGAGGTCTACTTTGTCCAGGCCACCCGCTCTCCAC		2726
Qy	2971	AGGGCTATATGAGCTGATGCTTGCTGTGAGCGGGGAGTCTGAGCAGCGACCCACT		3030
Db	2727	AGACCTGTATGAGCTGATGCTCCGCTGTGTGGAGCGGGAGCCCGAGCGAGCGCGCCT		2786
Qy	3031	TTTCCACACTCATTCGGTTCTCGGCAGAGATGCACTCAACAGCGTGTGAATCAACATCTC		3090
Db	2787	TCGCCCACTTCATTCGGTTCTCGGCGATATGCGTCAACACGGGTGAATCTCGAGCC		2846
Qy	3091	CAGCTGCC--CTCCCTAGGGAGTGAATCCAGGGGAGCCAGTGAACCTAAACAGAGAGA		3149
Db	2847	CGGAGCCCTTTCCCATATGGGAGGCATCCAGGGGAAGC--TGGATCTGAGAAACCGAATA		2904
Qy	3150	CACATGCGACACTTGCCCTTCCCTCCGACAGCCCATCAGCTTAATAGAGCATGA		3209
Db	2905	CGCTATGGCACCGACCCACCGCTTCATCACTTTC---CATTTCCAAAGGAGCATGT		2960
Qy	3210	GACTGACAGTGGGTGGGCCACCAAGAGAGTGAATGCCCTTCTCCCTCTTGGACAC		3269
Db	2961	CTGTGCGGGGTGGGCTGGGCGTGGCCGAGGAGCAGATACACACACT-----		3005
Qy	3270	ACTCTCATGTCCCTTCTCTGTCTCTCTCTCTGAAGACCCCTGTGTGCCACCCAGCTGT		3329
Db	3006	-----CCCTTCCGTTTCTTCTCTTCATCTGACCAGTGGCCACCCAGCTGTG		3054
Qy	3330	CCTGTGATGGAGTCTCTCCACCTTCCTTACCATCTCCTTGGGGAAGGGTGGGAGAA		3389
Db	3055	CTGTGTGGGATCTCTGCTGTGACTTCTTCCAGCTATCCCTTGGGGAAAGAACGGGGGAAA		3114
Qy	3390	ATATAGATAGACACTGGACATGGCCATTGGAGCACTGGGCGCCACTGTGACAACATG		3449

```
Db 3115 ATGCTGGAGTACTGGACA-----AGGCCCACTGGACAACACTG 3153
OY 3450 ATTCTGGAGAGGTGGCTGGCCCGAGCTTCTCTCCCTGCACACACTGGACCCACT 3509
    ||||| - ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3154 GTTCCGAGAGGTGAGTGCCCGCC--CAGCTTCTCTGTGCACACTGGACGCC 3211
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3510 GGCTGAGAAFTCTG-6GGGTGAGAGAGACAAGAGAGAAATGTTCTTGCTG 3568
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3212 AGCTGAGAAFTGAGAGGGGTGAGGGGACAAAGACG-----GCCAA 3251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3569 CTCCTGACTTGTCCCTCAGCTTGGGCTTCTCTCTCCATCAGCTGAACACTGGACCT 3628
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3252 CCCCTACACCGGGTCCCTCAGCCCTGCTCTCTGTTCCGCCCTGACACACTGGACCT 3311
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3629 GGGGTAGCCCGGCC-----CAGCCCTCAGTACACCCCACTTCCCACTTGCAGTCTG 3682
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3312 GGGGGCGATCCCTGCCGTGATCTGATCAGTACACACCCCTCTCCACCTGCCATGCTA 3371
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3683 TAGTAGAACTTCTTAAGCTATAGCTTCTGTGAGTAAATATGGATTTGGGGGAA 3742
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3372 CAGTAGAACTTCGCAAGCCCTCTATGTTCTGTGAGAAATATTAG---ATGGGGAAC 3428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3743 AGAGGAGCAACGCCCATAGCCTTGGGTTGGACATCTCTAGTGTAGCTGCCACATGA 3802
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3429 AGAGGAGCAATAGCTTGAGGC--TGGGGGTGGGATTTCTATTGACTACACATGG 3486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3803 TTTTCTATATCAGTTGGGTTTGTACATTTT---GGGGGAGAGACACAGATTTTA 3859
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3487 TTTTCTATATCAGCGGGTTTGTACATTTTGTGGGGAGAGAAACACAGATTTTA 3546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3860 CACTATATATGACCTAGACTTGAAGCAATTTAATCCCTGCAGTAGGCAAGTAAAT 3919
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3547 CACTATATATGAGACTAGCTTAAGCGCATTTTAATCCCTGCTAGGCAAGTAAAT 3606
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 3920 AAAGTTGAGTTT 3933
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3607 AAAGTTGAGTTGT 3620
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: October 5, 2002, 18:11:24
Job time: 15801 sec